### STIC-Biotech/ChemLib

Whiteman, Brian

From: Sent: Monday, March 07, 2005 7:20 AM

STIC-Biotech/ChemLib To:

Subject: seq search

09/475,704 Barnett et al. 12/30/99

SEQ ID NO: 3 and 4

Please search protein and NA databases

- default
   interference

Thank you,

Brian Whiteman Remsen, 2D14 mail box 2C18 Patent Examiner - Art Unit 1635 United States Patent and Trademark Office (571) 272-0764

STAFF USE ONLY Searcher:\_ Searcher Phone: 2-Date Searcher Picked up:\_ Date Completed:\_ Searcher Prep/Rev. Time:\_ Online Time:\_

Type of Search NA Sequence: #\_ AA Sequence :#\_ Structure: #\_ Bibliographic: Litigation:\_ Patent Family:\_ Other:

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Vendors and cost where applicable DIALOG: QUESTEL/ORBIT:\_ LEXIS/NEXIS:\_\_\_ SEQUENCE SYSTEM:\_ WWW/Internet:\_\_ Other(Specify):\_

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Maximum Match 100%
Listing first 45 summaries
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1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*

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No.	Score	Query Match	Query Match Length DB	DB	ID	Description
_	1509	100.0	1509	10	US-09-899-575-4	Sequence 4,
ผ	1507.4	99.9	1509	10	US-09-967-464-64	Sequence 64
w	1504.2	99.7	1509	10	US-09-967-464-68	Sequence 68,
4	1489.8	98.7	1509	10	US-09-899-575-21	Sequence 21
ហ	1297.6	86.0	1494	10	US-09-899-575-51	
თ	1294.8	85.8	1491	10	US-09-899-575-99	Sequence 99,
7	1276.8	84.6	1479	10	US-09-967-464-63	Sequence 63,
8	1276.8	84.6	1479	10	US-09-899-575-3	ω ,
9	1275.2	84.5	3162	15	US-10-190-435-18	Sequence 18, Appl
. 10	1275.2	84.5	3462	15	US-10-190-435-16	16,
11	1275.2	84.5	4419	15	US-10-190-435-19	19,

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## ALIGNMENTS

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Sequence 4, Application US/0989575;
Publication No. US20030223961A1
; GENERAL INFORMATION:
APPLICANT: Zur Megede, Jan
; APPLICANT: Barnett, Susan W.
APPLICANT: Egnelbrecht, Susan
APPLICANT: Egnelbrecht, Susan
APPLICANT: van Rensburg, Estrelita Janse
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
TITLE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF
FILE REFERENCE: PP01631.102
; CURRENT APPLICATION NUMBER: US/09/899,575
CURRENT FILING DATE: 2001-07-05
PRIOR APPLICATION NUMBER: 09/475,704
PRIOR APPLICATION NUMBER: 09/475,704
PRIOR FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 135
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 1509
TYPE: DNA
ORGANISM: Artificial Sequence
PEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic Gag
OTHER INFORMATION: of HIV strain AF110967
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Sequence 64, Application US/09967464

Publication No. US20030138453A1

GENERAL INFORMATION:

APPLICANT: O'Hagan, Derek

APPLICANT: Octen, Gillis

APPLICANT: Octen, Gillis

APPLICANT: Donnelly, John J.

APPLICANT: Barnett, Susan

APPLICANT: Dubensky, John J.

APPLICANT: Mamohan

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APPLICANT: APPLICATION NUMBER: US/09/967,464

CURRENT FILING DATE: 2000-09-28

PRIOR APPLICATION NUMBER: 60/236,105

PRIOR APPLICATION NUMBER: 60/315,905

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Sequence 68, Application US/09967464

Publication No. US20030138453A1

GENERAL INFORMATION:

APPLICANT: O'Hagan, Derek

APPLICANT: Otten, Gillis

APPLICANT: Donnelly, John J.

APPLICANT: Barnett, Susan

APPLICANT: Ulmer, Jeffrey

APPLICANT: Dubensky, Jr., Thomas W.

TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY OF 1

FILE REFERENCE: PP16269.004

CURRENT APPLICATION NUMBER: US/09/967,464

CURRENT APPLICATION NUMBER: 60/236,105

PRIOR APPLICATION NUMBER: 60/236,105

PRIOR APPLICATION NUMBER: 60/236,105

PRIOR APPLICATION NUMBER: 60/315,905

PRIOR FILING DATE: 2000-09-28

PRIOR FILING DATE: 2001-08-30

NUMBER OF SEQ ID NOS: 68

COUNTAINE: DESCRIPTION SERVERS OF 3 1
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; LENGTH: 1509
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; ORGANISM: Human immunodeficiency virus type
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US-09-899-575-51

US-09-899-575-51

Sequence 51, Application US/09899575

Publication No. US20030223961A1

GENERAL INFORMATION:

APPLICANT: Engelbrecht, Susan W.

APPLICANT: Engelbrecht, Susan W.

APPLICANT: Van Rensburg, Estrelita Janse

ITITLE OF INVENTION: POLYMUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C

TITLE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF

FILE REFERENCE: PP01631.102

CURRENT APPLICATION NUMBER: US/09/899,575

CURRENT FILING DATE: 2001-07-05

PRIOR APPLICATION NUMBER: 09/475,704

PRIOR APPLICATION NUMBER: 09/475,704

PRIOR FILING DATE: 1999-12-30

NUMBER OF SEQ ID NOS : 135

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 51

LENGTH: 1494

TYPE: DNA

OTHER INFORMATION: Description of Artificial Sequence: HIV Type C

OTHER INFORMATION: Gag optimized
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Best Local Sim
Matches 1402;
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Pred. No. 1.3e-271;
0; Mismatches 89; I
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RESULT 6
US-09-899-575-99
; Sequence 99, Application US/09899575
; Publication No. US20030223961A1
; GENERAL INFORMATION:
; APPLICANT: Zur Megede, Jan
; APPLICANT: Barnett, Susan W.
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APPLICANT: Egnelbrecht, Susan
APPLICANT: van Rensburg, Estrelita Janse
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
TITLE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF
FILE REFERENCE: PP01631.102
CURRENT APPLICATION NUMBER: US/09/899,575
CURRENT FILING DATE: 2001-07-05
PRIOR APPLICATION NUMBER: 09/475,704
PRIOR APPLICATION NUMBER: 09/475,704
PRIOR FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 135
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 99
LENGTH: 1491
TYPE: DNA
ORGANISM: Artificial Sequence
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; OTHER INFORMATION:
US-09-899-575-99
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Best Local Similarity 92.7%;
Matches 1401; Conservative
CAGGAGCAGATCGCCTGGATGACCAGCAACCCCCCCGTGCCCGTGGGCGACATCTACAAG
                                                                                                      GCCCCCGGCCAGATGCGCGACCCCCCCGCGGCACCAGCACCCTG
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Pred. No. 5.2e-271;
0; Mismatches 87; I
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WS-09-967-464-63

US-09-967-464-63

Sequence 63, Application US/09967464

Publication No. US20030138453A1

GENERAL INFORMATION:

APPLICANT: O'Hagan, Derek

APPLICANT: Otten, Gillis

APPLICANT: Donnelly, John J.

APPLICANT: Donnelly, John M.

APPLICANT: Barnett, Susan

APPLICANT: Barnett, Susan

APPLICANT: Singh, Mamohan

APPLICANT: Ulmer, Jeffrey

APPLICANT: Dubensky, Jr., Thomas W.

TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY OF

FILE REFERENCE: PP16269.004

CURRENT APPLICATION NUMBER: US/09/967,464

PRIOR APPLICATION NUMBER: 60/236,105
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CTGGACATCCGCCAGGGCCCCAAGGAGCCCTTCCGCGACTACGTGGACCGCTTCTTCAAG
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; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 60/315,90
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
; LENGTH: 1479
; TYPE: DNA
; ORGANISM: Human immunodeficiency vUS-09-967-464-63
                                                                                                                                                                                                                                                                                                                                   GCCGAC---GGCAAGGTGAGCCAGAACTACCCCATCGTGCAGAACCTGCAGGGCCAGATG
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Pred. No. 4.1e-267;
0; Mismatches 77; I
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897 840 837 777

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Sequence 3, Application US/0989575
; Publication No. US20030223961A1
; GENERAL INFORMATION:
    APPLICANT: Zur Megede, Jan
    APPLICANT: Barnett, Susan W.
    APPLICANT: Egnelbrecht, Susan
    APPLICANT: Egnelbrecht, Susan
    APPLICANT: Van Rensburg, Estrelita Janse
    TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
    TITLE OF INVENTION: POLYNEPTIDES, POLYPEPTIDES AND USES THEREOF
    FILE REFERENCE: PP01631.102
CURRENT APPLICATION NUMBER: US/09/899,575
CURRENT APPLICATION NUMBER: US/09/899,575
CURRENT APPLICATION NUMBER: 09/475,704
PRIOR APPLICATION NUMBER: 09/475,704
PRIOR FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 135
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 1479
TYPE: DNA
COTHER INFORMATION: Description of Artificial Sequence: synthetic Ga;
COTHER INFORMATION: of HIV strain AF110965
US-09-899-575-3
         Sn
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US-09-899-575-3
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pred. No. 4.1e-267; 
0; Mismatches 77; Indels 36;
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897

840 837 780 777 720 717 660 657 600 597 540 537 480 477 420 417 360 360

900

Query Match  B4.5%; Score 1275.2; DB 15; Length 3162; Best Local Similarity 92.5%; Pred. No. 8.9e-267;  Matches 1398; Conservative 0; Mismatches 78; Indels 36; Gaps 4;  Qy 1 ATGGGCCCCGCCCAGCATCCTGCGCGCGAGAAGCTGGACAAGTGGGAGAAGATCCGC 60	; TYPE: DNA ; ORGANISM: Artificial Sequence ; FEATURE: ; FEATURE: ; OTHER INFORMATION: Description of Artificial Sequence: GagRTmut_C US-10-190-435-18	CURRENT FILING DATE: 2002-12-30 NUMBER OF SEQ ID NOS: 319 SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 18 LENGTH: 3162	APPLICANT: ENGELBRECHT, SUBAN APPLICANT: VAN RENSBURG, Estrelita J. TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C TITLE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF FILE REFERENCE: PP18133.003 / 2302-18133 CHREENT APPLICATION NUMBER: US/10/190.435	GENERAL INFORMATION:  APPLICANT: ZUR MEGEDE, Jan  APPLICANT: BARNETT, Susan W.  APPLICANT: LIAN. Ying	RESULT 9 US-10-190-435-18 ; Sequence 18, Application US/10190435 ; Publication No. US20030143248A1	468 CTGAGCCAGTAA 14	1420	1378 CCCCCGCCGAGAGCTTCCGCTTCGAGGAGACCACCCCCCCC	1318 CGCCCCGCCACTTCCTGCAGAACCGCAGCCAGCCGCCCCCCCC	1258 AAGGACTGCACCGAGCGCCAGGCCAACTTCCTGGGCAAGATCTGGCCCAGCCACAAGGGC 131	1198 AACTGCCGCGCCCCCGCAAGAAGGCTGCTGGAAGTGCGGCAAGGAGGCCACCAGATG 125	1138 AAGGGCCCCGGCGAACGTCAAGTGCTTCAACTGCGGCAAGGAGGGCCACATCGCCAAG 119	1078 CTGGCCGAGGCGATGAGCCAGGCCAACAGCGTGAACATCATGATGCAGAAGAGCAACTTC 113	1018 CTGGAGGAGATGATGACCGCCTGCCAGGGCGTGGGCGGCCCCGGCCAAAGGCCCGCGTG 107
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Sequence 16, Application US/10190435
; Publication No. US20030143248A1
; GENERAL INFORMATION:
APPLICANT: ZUR MEGEDE, Jan
; APPLICANT: BARNETT, Susan W.
APPLICANT: BARNETT, Susan W.
APPLICANT: LIAN, Ying
; APPLICANT: VAN RENSBURG, Estrelita J.
; APPLICANT: VAN RENSBURG, Estrelita J.
; TITLE OF INVENTION: POLYMUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
TITLE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF
FILE REFERENCE: PP18133.003 / 2302-18133
; CURRENT APPLICATION NUMBER: US/10/190,435
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 319
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 16
; LENGTH: 3462
; TYPE: DNA
; ORGANISM: Artificial Sequence
; PEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: GagProtInaRTmut_C
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1378 CCCCCCGCCGAGAGCTTCCGCTTCGAGGAGACCACCCCCCCAAGCAGGAGCCCAAG 1	CCGCGCCCCCCGCAAGAAGGGCTGCTGGAAGTGCGGCAAGGAGGACCACC		୭ ପ୍—ପୁ ଉ—ହ	787 AAGCGGTGGATCATCCTGGGCCTGAACAAGATCGTGCGGATGTACAGCCCCGTGAGCATC  838 CTGGACATCCGCCAGGGCCCCAAGGAGCCCTTCCGCGACTACGTGGACCGCTTCTTCAAG	658 GTGGCCCCGGCCAGATGCGCGACCCCCCGCGGCAGCATCGCCGGCCACCACCACCACCACCACCACCACCACCACCAC	B GCCTTCAGCCCCGAGGTGATCCCCCATGTTCACCGCCCTGAGCGAGGGCGCCACCCCCAG

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RESULT 12
US-10-190-305A-14
; Sequence 14, Application US/10190305A
; Publication No. US20030198621A1
; GENERAL INFORMATION:
   APPLICANT: ZUR MEGEDE, Jan
   APPLICANT: BARNETT, Susan
; APPLICANT: LIAN, Ying
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE B AND/OR
   TITLE OF INVENTION: TYPE C POLYPEPTIDES, POLYPEPTIDES' AND USES THEREOF
; FILE REFERENCE: 2302-18702 / 18702.002
; CURRENT APPLICATION NUMBER: US/10/190,305A
; CURRENT FILING DATE: 2002-07-05
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: Patentin Ver. 2.0
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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: GagRTmutTatRevNef_C
US-10-190-305A-14
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                                                                                                        GCCTTCAGCCCCAGGTGATCCCCCATGTTCACCGCCCTGAGCGAGGGGGCGCCACCCCCAG
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RESULT 13

US-10-190-435-35

; Sequence 35, Application US/10190435
; Publication NO. US20030143248A1
; GENERAL INFORMATION:
; APPLICANT: ZUR MEGEDE, Jan
; APPLICANT: BARNETT, Susan W.
; APPLICANT: LIAN, Ying
; APPLICANT: ENGELBRECHT, Susan
; APPLICANT: VAN RENSBURG, Estrelita J.
; TITLE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF
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; FILE REFERENCE: PP18133.003 / 2302-18133; CURRENT APPLICATION NUMBER: US/10/190,435; CURRENT FILING DATE: 2002-12-30; NUMBER OF SEQ ID NOS: 319; SOFTWARE: PatentIn Ver. 2.0; SEQ ID NO 35; LENGTH: 4483; TYPE: DAA; ORGANISM: Artificial Sequence; FEATURE: OTHER INFORMATION: Description of Artificial Sequence; OTHER INFORMATION: gp160mod.TV1.dV1V2-gagmod.BW: US-10-190-435-35
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Best Local Similarity
Matches 1398; Conserv
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Pred. No. 8.7e-267;
0; Mismatches 78; I
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                                                                                 Sequence 34, Application US/10190435
; Dublication No. US20030143248A1
; GENERAL INFORMATION:
; APPLICANT: ZUR MEGEDE, Jan
APPLICANT: BARNETT, Susan W.
APPLICANT: LIAN, Ying
; APPLICANT: ENGELBRECHT, Susan
; APPLICANT: VAN RENSBURG, Estrelita J.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV T
TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES AND USES THE
FILE REFERENCE: PP18133.003 / 2302-18133
; CURRENT APPLICATION NUMBER: US/10/190,435
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 319
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 34
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LENGTH: 4606
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description
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Pred. No. 8.7e-267;
0; Mismatches 78; I
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                                                                                                                                                                                                                                Sequence 36, Application US/10190435;
Publication No. US20030143248A1
; GENERAL INFORMATION:
APPLICANT: ZUR MEGEDE, Jan
APPLICANT: BARNETT, Susan W.
APPLICANT: LIAN, Ying
APPLICANT: LIAN, Ying
APPLICANT: VAN RENSBURG, Estrelita J.
APPLICANT: VAN RENSBURG, Estrelita J.
APPLICANT: VAN RENSBURG, ESTRELITES ENCODING ANTIGENIC HIV TYPE C
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
TITLE REFERENCE: PP18133.003 / 2302-18133
; CURRENT APPLICATION NUMBER: US/10/190,435
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 319
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 36
; LENGTH: 4615
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                                                                                                                                          ; OTHER INFORMATION: Description of Artificial Sequence: ; OTHER INFORMATION: gp160mod.TV1.dV2-gagmod.BW965 US-10-190-435-36
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                ATGGGCGCCCCGCCAGCATCCTGCGCGGCGGCAAGCTGGACGCCTGGGAGCGCATCCGC
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                                                                          Score 1275.2; DB 19
Pred. No. 8.7e-267;
0; Mismatches 78;
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4615;

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СТGAGCCAGTAA 1509              СТGAGCCAATAA 4615	GACCGCGAGCCCTACCGCGAGCCCCTGACCGCCCTGCGCAGCCTGTTCGGCAGCGGCCCC	CCCCCCGCCGAGAGCTTCCGCTTCGAGGAGACCACCCCCGCCCCAAGCAGGAGGAGCCAAG	CGCCCCGGCAACTTCCTGCAGAACCGCAGCGAGCCCGCCGCCCCCCCC	AAGGACTGCACCGAGCGCCAGGCCAACTTCCTGGGCAAGATCTGGCCCAGCCACAAGGGC	AACTGCCGCGCCCCCCCCAAGAAGGGCTGCTGGAAGTGCGGCAAGGAGGGCCACCAGATG	
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Search completed: March 13, 2005, 04:29:43 Job time : 923.106 secs

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No.

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-Q=/cgn2 1/USPTO spool p/US09475704/runat 10032005 140224 14937/app query.fasta_1.3342
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-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
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-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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# ALIGNMENTS

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WS-09-899-575-22

US-09-899-575-22

; Sequence 22, Application US/09899575

; Publication No. US20030223961A1

; GENERAL INFORMATION:

; APPLICANT: Zur Megede, Jan

; APPLICANT: Barnett, Susan

; APPLICANT: Beneburg, Estrelita Janse

TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C

TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C

TITLE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF

FILE REFERENCE: PP01631.102

CURRENT APPLICATION NUMBER: US/09/899,575

CURRENT FILING DATE: 2001-07-05

PRIOR APPLICATION NUMBER: 09/475,704

PRIOR APPLICATION NUMBER: 09/475,704

PRIOR FILING DATE: 1999-12-30

NUMBER OF SEQ ID NOS: 135

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 22

LENGTH: 502

TYPE: PRT

ORGANISM: Human immunodeficiency virus
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Result

Query

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CTGCGCGCGAGCAGGCCACCCAGGACGTGAAGAACTGGATGACCGAGACCCTGCTGGTG
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                              Sequence 2, Application US/10332413

Publication No. US20040116660A1

GENERAL INFORMATION:

APPLICANT: Johnstone, Robert Edward

APPLICANT: Swanstrom, Ronald Ivar

APPLICANT: Swanstrom, Ronald Ivar

APPLICANT: Morris, Lynn

APPLICANT: Williamson, Carolyn

TITLE OF INVENTION: Process for the Selection of HIV-1 Subtype C Isolates, Selected H

TITLE OF INVENTION: Subtype Isolates, Their Genes nd Modifications and Derivatives T:

FILE REFERENCE: 45669-281993

CURRENT APPLICATION NUMBER: US/10/332,413

CURRENT APPLICATION NUMBER: PCT/IB01/01208

PRIOR APPLICATION NUMBER: US 60/216,995

PRIOR APPLICATION NUMBER: US 60/216,995

PRIOR APPLICATION NUMBER: ZA 2000/3437

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-07-10

PRIOR FILING DATE: 2000-09-15

NUMBER OF SEQ ID NOS: 32

SOFTWARE: Patentin version 3.1

SEQ ID NOS: 32

ILENGTH: 402
; LENGTH: 492
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-332-413-2
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Percent Similarity:
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Query Match:
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RESULT 3
US-09-991-258-5
; Sequence 5, Application US/09991258
; Patent No. US20020141975A1
; GENERAL INFORMATION:
APPLICANT: Olmsted, Robert
APPLICANT: Caley, Ian
APPLICANT: Caley, Ian
APPLICANT: Johnston, Robert
APPLICANT: Johnston, Robert
APPLICANT: Johnston, Robert
APPLICANT: Johnston, Robert
APPLICANT: Swanstrom, Ronald
TITLE OF INVENTION: ALPHAVIRUS VECTORS ANI
TITLE OF INVENTION: VACCINES
FILE REFERENCE: 01113.0001U3
CURRENT APPLICATION NUMBER: US/09/991,258
CURRENT FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: 60/216,995
PRIOR APPLICATION NUMBER: 60/216,995
PRIOR APPLICATION NUMBER: 60/216,995
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PRIOR APPLICATION NUMBER: 6
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Sequence 8, Application US/10332413

Publication No. US20040116660A1

REPLICANT: Johnstone, Robert Edward
APPLICANT: Warnstrom, Ronald Ivar
APPLICANT: Williamson, Carolyn
TITLE OF INVENTION: Subtype Isolates, Their Genes nd Modifications and Derivatives T
FILE REFERENCE: 45569-281993
CURRENT PILLE OF INVENTION: Subtype Isolates, Their Genes nd Modifications and Derivatives T
FILE REFERENCE: 45569-281993
CURRENT PILLING DATE: 2003-09-12
PRIOR APPLICATION NUMBER: US/10/332,413
CURRENT PILLING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: US 60/216,995
PRIOR FILLING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: ZA 2000/3437
PRIOR PILLING DATE: 2000-09-15
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin version 3.1
SEQ ID NO 8
LENGTH: 631
TYPE: PRT
US-10-332-413-8
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US-10-332-413-8
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Best Local Similarity:
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                 GlnGluGlnIleAlaTrpMetThrSerAsnProProIleProValGlyAspIleTyrLys
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                                        ArgTrpIleIleLeuGlyLeuAsnLysIleValArgMetTyrSerProValSerIleLeu
                                                   CGGTGGATCATCCTGGGCCTGAACAAGATCGTGCGGATGTACAGCCCCGTGAGCATCCTG
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Matches:
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US-10-339-217-109
US-10-339-217
Sequence 109, Application US/10339217
Publication No. US20030198648A1
GENERAL INFORMATION:
APPLICANT: Buechter, Douglas
APPLICANT: Hou, Xiaohong
APPLICANT: Marlor, Christopher W.
APPLICANT: Rice, William G.
APPLICANT: Yang, Wengang
TITLE OF INVENTION: Methods for Identifying Compounds Which Inhi
TITLE OF INVENTION: Nucleocapsid 7 Protein to HIV-1 RNA
FILE REFERENCE: 111021.143 (ACT-US1)
CURRENT APPLICATION NUMBER: US/10/339,217
CURRENT APPLICATION NUMBER: US/0/347,369
PRIOR APPLICATION NUMBER: US 60/347,369
PRIOR FILING DATE: 2002-01-11
NUMBER OF SEQ ID NOS: 144
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 109
LENGTH: 492
TYPE: PRT
ORGANISM: HIV-1
US-10-339-217-109
                                     Score:
                                                     Alignment Pred. No.:
Percent Similarity:
Best Local Similarity:
Query Match:
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US-10-339-217-109
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US-09-475-704A-4 (1-1509) x US-10-339-217-109 (1-492)
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APPLICANT: Marlor, Christopher W.
APPLICANT: Rice, William G.
APPLICANT: Yang, Wengang
TITLE OF INVENTION: Methods for Identifying Confilte Reference: 111021.143 (ACH-US1)
CURRENT APPLICATION NUMBER: US/10/339,217
CURRENT FILING DATE: 2003-01-09
PRIOR APPLICATION NUMBER: US 60/347,369
PRIOR APPLICATION NUMBER: US 60/347,369
PRIOR FILING DATE: 2002-01-11
NUMBER OF SEQ ID NOS: 144
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 110
                                                                                                                                                                         ; LENGTH: 492
; TYPE: PRT
; ORGANISM: HIV-1
US-10-339-217-110
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US-10-339-217-140

; Sequence 140, Application US/10339217
; Publication No. US20030198648A1
; GENERAL INFORMATION:
; APPLICANT: Buechter, Douglas
; APPLICANT: Hou, Xiaohong
; APPLICANT: Marlor, Christopher W.
; APPLICANT: Rice, William G.
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APPLICANT: Marlor, Christopher W.
APPLICANT: Rice, William G.
APPLICANT: Rice, William G.
APPLICANT: Yang, Wengang
TITLE OF INVENTION: Methods for Identifying Co:
FILE REFERENCE: 111021.143(ACH-US1)
CURRENT APPLICATION NUMBER: US/10/339,217
CURRENT FILING DATE: 2003-01-09
PRIOR APPLICATION NUMBER: US 60/347,369
PRIOR PILING DATE: 2002-01-11
NUMBER OF SEQ ID NOS: 144
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 140
LENGTH: 491
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Best Local Similarity:
Query Match:
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; ORGANISM: HIV-1
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TGCCGCGCCCCCCGCAAGAAGGGCTGCTGGAAGTGCGGCAAGGAGGGCCCACCAGATGAAG 1260
                                   GCCGAGGCGATGAGCCAAGGCCAACAGCGTGAACATCATGATGCAGAAGAAGAGCAACTTCAAG
                                                                                                                         GAGGAGATGATGACCGCCTGCCAGGGCGTGGGCGGCCCCGGCCACACAAGGCCCCGCGTGCTG
                                                                        AlaGluAlaMetSerGlnThrAsnSer---ThrIleLeuMetGlnArgSerAsnPheLys
                                                                                                             GlnAsnAlaAsnProAspCysLysThrIleLeuArgAlaLeuGlyProGlyAlaSerLeu
                                                                                                                                                           CAGAACGCCAACCCCGACTGCAAGACCATCCTGCGCGCTCTCGGCCCCGGCGCGCCACCCTG
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RESULT 8
US-10-339-217-143
; Sequence 143, Application US/10339217
; Publication No. US20030198648A1
; GENERAL INFORMATION:
   APPLICANT: Buechter, Douglas
; APPLICANT: Hou, Xiaohong
; APPLICANT: Marlor, Christopher W.
   APPLICANT: Yang, Wengang
; TITLE OF INVENTION: Methods for Identifying Com
   TITLE OF INVENTION: Nucleocapsid 7 Protein to
   FILE REFERENCE: 111021.143 (ACH-US1)
; CURRENT APPLICATION NUMBER: US/10/339,217
; CURRENT FILING DATE: 2003-01-09
; PRIOR APPLICATION NUMBER: US 60/347,369
; PRIOR FILING DATE: 2002-01-11
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 143
; TYPE: PRT
   OPGRANTSM: UTV.1
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US-10-339-217-143
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                                                                                  TGCCGCGCCCCCGCAAGAAGGGCTGCTGGAAGTGCGGCAAGGAGGGCCCACCAGATGAAG
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APPLICANT: Buechter, Douglas
APPLICANT: Hou, Xiaohong
APPLICANT: Marlor, Christopher W.
APPLICANT: Marlor, Christopher W.
APPLICANT: Marlor, Christopher W.
APPLICANT: Yang, Wengang
TITLE OF INVENTION: Methods for Identifying Com
TITLE OF INVENTION: Nucleocapsid 7 Protein to
FILE REFERENCE: 111021.143 (ACH-US1)
CURRENT APPLICATION NUMBER: US/10/339,217
CURRENT APPLICATION NUMBER: US 60/347,369
PRIOR APPLICATION NUMBER: US 60/347,369
PRIOR FILING DATE: 2002-01-11
NUMBER OF SEQ ID NOS: 144
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 105
LENGTH: 508
TYPE: PRT
ORGANISM: HIV-1
US-10-339-217-105
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Query Match:
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US-10-339-217-105
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                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                                                                       Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 105, Application No. US20 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                               No.:
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Matches:
Conservative:
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Binding

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                                                                                        GlyArgProGlyAsnPheLeuGlnAsnArgProGluProThrAlaProProAlaGluSer
                                                                                                           ATGAAGGACTGCACCGAGCGCCAAGCTTCCTGGGCAAGATCTGGCCCAGCCACAAG 1314
                              PheArgAsnArgProGluProThrAlaProProAlaGluSerPheArgPheGluGluThr
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; Publication No. US20030198648A1

; GENERAL INFORMATION:

APPLICANT: Buechter, Douglas
APPLICANT: Hou, Xiaohong

APPLICANT: Marlor, Christopher W.

; APPLICANT: Yang, Wengang

TITLE OF INVENTION: Methods for Identifying Cor

TITLE OF INVENTION: Nucleocapsid 7 Protein to

FILE REFERENCE: 111021.143(ACH-US1)

CURRENT APPLICATION NUMBER: US/10/339,217

CURRENT FILING DATE: 2003-01-09

PRIOR APPLICATION NUMBER: US 60/347,369

PRIOR FILING DATE: 2002-01-11

NUMBER OF SEQ ID NOS: 144

SOFTWARE: FastSEQ for Windows Version 4.0

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Sequence 107, Application US/10339217

Publication No. US20030198648A1

GENERAL INFORMATION:

APPLICANT: Buechter, Douglas

APPLICANT: Hou, Xiaohong

APPLICANT: Marlor, Christopher W.

APPLICANT: Rice, William G.

APPLICANT: Rice, William G.

APPLICANT: Nang, Wengang

TITLE OF INVENTION: Mucleocapsid 7 Protein to

FILE REFERENCE: 111021.143(ACH-US1)

CURRENT APPLICATION NUMBER: US/10/339,217

CURRENT FILING DATE: 2003-01-09

PRIOR APPLICATION NUMBER: US 60/347,369

PRIOR FILING DATE: 2002-01-11

NUMBER OF SEQ ID NOS: 144

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 107

LENGTH: 497

TYPE: PRT

OPCANISM: HIV-1
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Best Local Similarity:
Query Match:
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US-10-339-217-107
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RESULT 12
US-10-339-217-106
Sequence 106, Application US/10339217
Publication No. US20030198648A1
GENERAL INFORMATION:
APPLICANT: Buechter, Douglas
APPLICANT: Hou, Xiaohong
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APPLICANT: Rice, William G.
APPLICANT: Yang, Wengang
TITLE OF INVENTION: Methods for Identifying Co.
FILE REFERENCE: 111021.143 (ACH-US1)
CURRENT APPLICATION NUMBER: US/10/339,217
CURRENT FILING DATE: 2003-01-09
PRIOR APPLICATION NUMBER: US 60/347,369
PRIOR FILING DATE: 2002-01-11
NUMBER OF SEQ ID NOS: 144
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 106
LENGTH: 487
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; ORGANISM: HIV-1
US-10-339-217-106
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                                AspLeuAsnThrMetLeuAsnThrValGlyGlyHisGlnAlaAlaMetGlnMetLeuLys
                                                                            GACCTGAACACGATGTTGAACACCGTGGGCGGCCACCAGGCCGCCATGCAGATGCTGAAG
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RESULT 13
US-10-339-217-108
; Sequence 108, Application US/10339217
; Publication No. US20030198648A1
; GENERAL INFORMATION:
   APPLICANT: Buechter, Douglas
; APPLICANT: Hou, Xiaohong
; APPLICANT: Marlor, Christopher W.
; APPLICANT: Rice, William G.
; TITLE OF INVENTION: Methods for Identifying Compounds Which Inhibit Bind; TITLE OF INVENTION: Nucleocapsid 7 Protein to HIV-1 RNA
; CURRENT APPLICATION NUMBER: US/10/339,217
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; ORGANISM: HIV-1
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PRIOR APPLICATION NUMBER: US 60/347,369
PRIOR FILING DATE: 2002-01-11
NUMBER OF SEQ ID NOS: 144
SOFTWARE: FastSEQ for Windows Version 4.
SEQ ID NO 108
LENGTH: 496
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RESULT 14
US-09-899-575-17
; Sequence 17, Application US/09899575
; Publication No. US20030223961A1
; GENERAL INFORMATION:
APPLICANT: Zur Megede, Jan
APPLICANT: Barnett, Susan W.
APPLICANT: Begnelbrecht, Susan
APPLICANT: van Rensburg, Estrelita Janse
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV
TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES AND USES TH
FILE REFERENCE: PP01631.102
CURRENT APPLICATION NUMBER: US/09/899,575
CURRENT FILING DATE: 2001-07-05
PRIOR APPLICATION NUMBER: 09/475,704
PRIOR FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 135
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 17
LENGTH: 492
TYPE: PRT
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Human immunodeficiency virus US-09-899-575-17
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            CTGGACATCCGCCAGGGCCCCAAGGAGCCCTTCCGCGACTACGTGGACCGCTTCTTCAAG
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                                                                                          LeuGlnGluGlnIleAlaTrpMetThrSerAsnProProIleProValGlyAspIleTyr
                                                                                                     CTGCAGGAGCAGATCGCCTGGATGACCAGCAACCCCCCCGTGCCCGTGGGCGACATCTAC
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Sequence 18, Application US/10339217
; Publication No. US20030198648A1
; GENERAL INFORMATION:
APPLICANT: Buechter, Douglas
APPLICANT: Hou, Xiaohong
APPLICANT: Marlor, Christopher W.
APPLICANT: Rice, William G.
APPLICANT: Yang, Wengang
TITLE OF INVENTION: Methods for Identifying Com
TITLE OF INVENTION: Nucleocapsid 7 Protein to
FILE REFERENCE: 111021.143 (ACH-US1)
CURRENT APPLICATION NUMBER: US/10/339,217
CURRENT FILING DATE: 2003-01-09
PRIOR APPLICATION NUMBER: US 60/347,369
PRIOR FILING DATE: 2002-01-11
NUMBER OF SEQ ID NOS: 144
SOPTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
LENGTH: 500
TYPE: PRT
ORGANISM: HIV-1
US-10-339-217-18
                    Alignment Scores: Pred. No.:
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US-10-339-217-18
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 3.79e-108
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91.52%
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 Length:
Matches:
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IleGlyGlnLeuGlnProAlaValGlnThrGlySerGluGluLeuLy8SerLeuPheA8n
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                                   GCCGGCCCGTGGCCCCGGCCAGATGCGCGACCCCCGCGCAGCGACATCGCCGGCGGCCCC
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                                                     TTCTTCAAGACCCTGCGCGCGAGCAGGCCACCCAGGACGTGAAGAACTGGATGACCGAG
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474 GlnLysGlnGluGlnLysAsnGlnGluPro-----GlnProLeuThrSerLeuArgSer 491
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CTGTTCGGCAGCGGCCCCCTG 1500
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Search completed: March 11, 2005, 16:38:47 Job time : 210.272 secs

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Result
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-Q=/cgn2_1/USPTO_spool_p/US09475704/runat_10032005_140222_14851/app_query.fasta_1.3342
-DB=Issued_Patents_AA -QFMT=fastan -SUFFIX=n2p.rai -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09475704_@CGN_1_1_86_@runat_10032005_140222_14851 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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seq length: 2000000000
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1: /cgn2_6/ptodata/1
2: /cgn2_6/ptodata/1
3: /cgn2_6/ptodata/1
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Copyright (c) 1993 - 2005 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                         /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/pCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/pcKfIles1.pep:*
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           US-09-991-258-5
US-08-375-510-1
US-08-487-657-1
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US-09-952-060-35
US-08-463-210-8
US-09-124-900-2
US-08-463-028-8
US-08-816-1558-45
US-09-079-587-45
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16, Appl
16, Appl
35, Appli
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US-09-991-258-5
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# ALIGNMENTS

APPLICANT: Olmsted,

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; OTHER INFORMATION: Description of Artificial ; OTHER INFORMATION: synthetic construct US-09-991-258-5
                        Alignment Scores: Pred. No.:
                                                                                                                                                                                                                                                                                     APPLICANT: Davis, Nancy
APPLICANT: Swanstrom, Ronald
TITLE OF INVENTION: ALPHAVIRUS VECTORS AND V
TITLE OF INVENTION: VACCINES
FILE REFERENCE: 01113.0001U3
CURRENT APPLICATION NUMBER: US/09/991,258
CURRENT FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 09/902,537
PRIOR APPLICATION NUMBER: 60/216,995
PRIOR APPLICATION NUMBER: 60/216,995
PRIOR FILING DATE: 2000-07-07
NUMBER OF SEQ ID NOS: 19
COPTWANDE: Page SEC FOR Windows Version 4.0
                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 5
LENGTH: 492
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Keith, Paula
APPLICANT: Dryga, Sergey
APPLICANT: Caley, Ian
APPLICANT: Maughan, Maureen
APPLICANT: Johnston, Robert
APPLICANT: Davis, Nancy
APPLICANT: Swanstrom, Ronald
                                                                                                                                                          ORGANISM: Artificial Sequence FEATURE:
2.32e-141
2457.00
Length:
Matches:
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                                                                              AspileArgGinGlyProLysGluProPheArgAspTyrValAspArgPhePheLysThr
                                                                                             GACATCCGCCAGGGCCCCAAGGAGCCCTTCCGCGACTACGTGGACCGCTTCTTCAAGACC
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/375,510
FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/985,949
APPLICATION NUMBER: US/07/985,949
FILING DATE: 04-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Svensson, Leonard R.
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 216-309P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 241-1300
                                                                                                                                             STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
                                                                                                                                                                                                                                                                   APPLICANT: Saito, Atsushi
APPLICANT: Sinagawa, Hideo
APPLICANT: Nakata, Atsuo
TITLE OF INVENTION: HIV ANTIGEN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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; TELEFAX: (703) 241-2848
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 500 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Human immunodef:
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Pred. No.:
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                                                                                                                  GAGAAGGCCTTCAGCCCCGAGGTGATCCCCCATGTTCACCGCCCTGAGCGAGGGCGCCACC
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                                                                                                                                                                                                                                                                                                            Human immunodeficiency virus
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90.16%
83.66%
79.08%
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Matches:
Conservative:
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                                                                                                 Sequence 1, Application Patent No. 5834267 GENERAL INFORMATION:
                                               APPLICANT: Saito, Atsushi
APPLICANT: Sinagawa, Hideo
APPLICANT: Nakata, Atsuo
TITLE OF INVENTION: HIV ANTIGEN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Ster
STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22040-0747
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                                                                                                                  US/08487657
                                       Stewart,
                                          Kolasch
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                                          and
                                          Birch
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<pre>3InGluProIleAspLysGluLeuTyrProLeuAlaSerLeuArgSer 3GCAGCGGCCCCCTGAGCCAG 1506</pre>	23 AAGCAGGAGCCCAAGGACCGCGAGCCCTACCGCGAGCCCTGACCGCCCTGCGCAGCCTG	1369 CCCACCGCCCCCCCCCCGCGAGAGCCTTCCGAGGAGACCACCCCCCCCCC	CALAMAGGE CGCCCGGCAACTTCCTGCAGAACCGCAGCGAGCCCGCCCCCCACCGTG 	- AT CALCAGA I GAAGGAC CAACTICC TO GAGGA AGAT CTGGCCAGGAGAT CTGCCAGGAGAT CTGGCCAGGAGAT CTGGCCAGGAGAT CTGGCCAGGAGAT CTGGCCAGGAGAT CTGGCCAGGAGAT CTGGCCAGGAGAT CTGGCCAGGAGAT CTGGCCAGAGAT CTGGCCAGAT CTGGCCAGAGAT CTGGCCAGAGAT CTGGCCAGGAGAT CTGGCCAGAGAT CTGGCAGAGAT CTGGCCAGAGAT CTGCAGAGAT CTGCA	189 ATCGCCAAGAACTGCCGCGCCCCCCGCAAGAAGGGCTGCTGGAAGTGCGGCAAGGAGGGCCGCAAGGAGGGCCGCAAGAAGTGCGGCAAGGAGGGCCGCAAGGACGGCCGCAAGAAGTGCGGCAAGGAGGGCCGCAAGAAGTGCGGAAGTGCGGAAGGACGGCCAAGGAAGG	129 AGCAACTTCAAGGGCCCCCGGCGCAACGTCAAGTGCTTCAACTGCGGCAAGGAGGGCCAC        :::     :::	072 CGCGTGCTGGCCGAGGCGATGAGCCAGGCCAACAGCGTGAACATCATGATGCAGAAGAGCAGAAG 	41 AlaThrLeuGluGluMetMetThrAlaCysGlnGlyValGlyGlyProGlyHisLysAla	12 GCCACCCTGGAGGAGATGATGACCGCCTGCCAGGGCGTGGGCGGCCGGC	952 CTGCTGGTGCAGAACGCCAACCCCGACTGCAAGACCATCCTGCGCGCGC	1 TyrLysThrLeuArgAlaGluGlnAlaSerGlnGluValLysAsnTrpMetThr	erIleLeuAspIleArgGinGlyProLysGluProPheArgAspTyrValAspArgPhe	832 AGCATCCTGGACATCCGCCAGGGCCCCCAAGGAGCCCTTCCGCGACTACGTGGACCGCTTC 891	772 ATCTACAAGCGGTGGATCATCCTGGGCCTGAACAAGATCGTGCGGATGTACAGCCCCGTG 831	41 SerThrLeuGlnGluGlnIleGlyTrpMetThrHisAsnProProIleProValGlyGlu	GCACCCTGCAGGAGCAGATCGCCTGGATGACCAGCAACCCCCCGTGCCCCGTGGG	652 GGCCCCGTGGCCCCGGCCAGATGCGCCGACCCCCGCGGCAGCGACGCATCGCCGGCGCGCACC 711	:::	92 CTGAAGGACACCATCAACGAGGAGGCCGCCGAGTGGGACCCCCTGCACCCCCGTGCAGGCC	532 CCCCAGGACCTGAACACGATGTTGAACACCGTGGGCCGCCACCAGGCCGCCATGCAGATG 591	472 GAGAAGGCCTTCAGCCCCGAGGTGATCCCCATGTTCACCGCCCTGAGCGAGGGGGCGCCACC 531 	12 CAGATGGTGCACCAGGCCATCAGCCCCCGCACCCTGAACGCCTGGGTGAAGGTGATG 

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Sequence 16, Application US/09309572

Patent No. 6440730

GENERAL INFORMATION:
APPLICANT: Heinrich-Pette-Institut
ITITLE OF INVENTION: Retroviral hybrid vectors pse
FILE REFERENCE: P50489
CURRENT APPLICATION NUMBER: US/09/309,572
CURRENT FILING DATE: 1999-05-11
EARLIER APPLICATION NUMBER: DE 198 56 463
EARLIER FILING DATE: 1998-11-26
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 16
LENGTH: 500
TYPE: PRT
ORGANISM: Human immunodeficiency virus type 1
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OTHER INFORMATION:
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Sequence 16, Application US/09718096
Patent No. 6589763
GENERAL INFORMATION:
APPLICANT: Von Laer, Meike-Dorothe
TITLE OF INVENTION: RETROVIRAL HYB
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RETROVIRAL HYBRID VECTORS PSEUDOTYPED WITH LCMV
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; FILE REFERENCE: 35-195
; CURRENT APPLICATION NUMBER: US/09/718,096
; CURRENT FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: DE 19856463.5
; PRIOR FILING DATE: 1998-11-26
; PRIOR APPLICATION NUMBER: EP 99250415.9
; PRIOR FILING DATE: 1999-11-25
; PRIOR APPLICATION NUMBER: US 09/309,572
; PRIOR FILING DATE: 1999-05-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 500
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Score:
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Best Local Similarity:
Query Match:
DB:
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ORGANISM: Human
FEATURE:
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                                              AspThrGlyAsnAsnSerGlnValSerGlnAsnTyrProIleValGlnAsnLeuGlnGly
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; Sequence 35, Application US/09; Patent No. 6733993; GENERAL INFORMATION:
APPLICANT: Emini, Emilio A. APPLICANT: Evouil, Rima
APPLICANT: Bett, Andrew J. APPLICANT: Chen, Ling
APPLICANT: Kaslow, David C. APPLICANT: Shiver, John W. APPLICANT: Casimiro, Danilo
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TITLE OF INVENTION: ENHANCED FIRST GENERATION ADENOVIRUS
TITLE OF INVENTION: VACCINES EXPRESSING CODON OPTIMIZED HIV:
TITLE OF INVENTION: WODDIFICATIONS
FILE REFERENCE: 20747Y
CURRENT APPLICATION NUMBER: US/09/952,060
CURRENT FILING DATE: 2001-09-14
PRIOR APPLICATION NUMBER: PCT/US01/28861
PRIOR FILING DATE: 2001-09-14
PRIOR APPLICATION NUMBER: 60/317,814
PRIOR APPLICATION NUMBER: 60/279,056
PRIOR FILING DATE: 2001-09-07
PRIOR APPLICATION NUMBER: 60/279,056
PRIOR APPLICATION NUMBER: 60/279,056
PRIOR FILING DATE: 2001-03-27
PRIOR APPLICATION NUMBER: 60/233,180
PRIOR FILING DATE: 2000-09-15
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 35
LENGTH: 1350
TYPE: PRT
ORGANISM: Artificial Sequence
PEATURE:
OTHER INFORMATION: Codon optimized gag-IA pol fusion
US-09-952-060-35
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Best Local Similarity:
Query Match:
DB:
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 RESULT 7
US-08-463-210-8
; Sequence 8, Application US/08463210
; Patent No. 6001977
; GENERAL INFORMATION:
; APPLICANT: CHANG, Nancy T.
APPLICANT: GALLO, Robert C.
; APPLICANT: WONG-STAAL, Flossie
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CHANG, Nancy T.
GALLO, Robert C.
WONG-STAAL, Flossie
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Serunian, Leslie A.
REGISTRATION NUMBER: 35,353
REFERENCE/DOCKET NUMBER: 2026-4193US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEPHONE: (212) 751-6849
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 512 amino acids
TYPE: amino acids
TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY: linear
MOLECTIVE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 05-JUN-1995
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/693,866
FILING DATE: 23-JAN-1985
PRIOR APPLICATION NUMBER: US 06/659,339
APPLICATION NUMBER: US 06/659,339
FILING DATE: 10-OCT-1984
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version

CURRENT APPLICATION DATA:
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NAME/KEY:
                                                                                                                                                                                                                                                                                                                No::
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: Protein
LOCATION: 1.512
OTHER INFORMATION:
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CITY: New York
STATE: New York
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                                    ATGAAGCAGCTGCAGCCCCTGCAGACCGGCACCGAGGAGCTGCGCAGCCTGTACAAC
                                                               LeuGluArgPheAlaValAsnProGlyLeuLeuGluThrSerGluGlyCysArgGlnIle
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05-JUN-1995
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                        HisGlnMetLysAspCysThrGluArgGlnAlaAsnPheLeuGlyLysIleTrpProSer
                                                                          ThrAlaArgAsnCysArgAlaProArgLysLysGlyCysTrpLysCysGlyLysGluGly
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Qy 241 ACCGTGGCCACCCTGTACTGCGTGCACGCCGGCATCGAGGTCCGCGACACCAAGGAGGCC 300	Qy 181 ATGAAGCAGCTGCAGCCCGCCCTGCAGACCGGCACCGAGGAGCTGCGCAGCCTGTACAAC 240 :::          :::	Qy 121 CTGGAGGGCTTCGCCCTGAACCCCGGCCTGGTGGAGACCGGCGAGGGGCTGCAAGCAGATC 180             :::	Qy 61 CTGCGCCCCGGCGCAAGAAGCACTACATGCTGAAGCACCTGGTGTGGGCCCAGCCGCGAG 120	1 ATGGGCGCCCGCGCCAGCATCCTGCGCGGCGAG                 :::    1 MetGlyAlaArgAlaSerValLeuSerGlyGly	Y Match: 78.77% Indels: 3 Gaps: 9-475-704A-4 (1-1509) x US-09-124-900-2 (1-512)	Alignment scores:  4.99e-128 Length: 512  Score: 2237.00 Matches: 422  Percent Similarity: 89.69% Conservative: 39  Rest Local Similarity: 82.10% Mismatches: 39		SOFTWARE: Pater SEQ ID NO 2 LENGTH: 512	FILING DATE: 1998-07-30 PPLICATION NUMBER: PCT/EP95/0 ILING DATE: 1995-04-19 OF SEO ID NOS: 11	APPLICANT: MUSTER, Thomas TITLE OF INVENTION: HIV-Vaccines FILE REFERENCE: 1939-112P CURRENT APPLICATION NUMBER: US/09/124	APPLICANT: PREDL,  APPLICANT: SCHMATZ  APPLICANT: KLIMA,  APPLICANT: STEINDI	APPLICANT APPLICANT APPLICANT	Patent No. 6268484 GENERAL INFORMATION: APPLICANT: KATINGER, F	ESULT 8 S-09-124-900-	Qy 1465 ACCGCCTGCGCAGCCTGTTCGGCAGCGGCCCCCTGAGCCAG 1506    :::               :::           Db 499 ThrSerLeuArgSerLeuPheGlyAsnAspProSerSerGln 512	QY 1405 GAGACCACCCCCCCCAAGCAGGAGCCCAAGGACCCGCGAGCCCCTACCGCGAGCCCCTG 1464	QY 1369TTCGAG 1404	:::
. Oy	B 5	D K	S & S	Q dd Q	Db Qy	D Qy	Qy	D Q	Db Qy	p Q	D Q	D Q	B &	B &	D	S B 8	g b	<i>장</i> 음
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Percent Similarity:
Best Local Similarity:
                                       Alignment Scores: Pred. No.:
                           Score:
                                                                               US-08-463-028-8
                                                                                                                                                                                                                                 NAME: Serunian, Leslie A.
REGISTRATION NUMBER: 35,353
REFERENCE/DOCKET NUMBER: 2026-4193US3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 512 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 345 Park Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10154-0053
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,028
                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/693,86
FILING DATE: 23-JAN-1985
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/659,33
FILING DATE: 10-OCT-1984
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: CHANG, Nancy T.
APPLICANT: GALLO, Robert C.
APPLICANT: WONG-STAAL, Flossie
TITLE OF INVENTION: CLONING AND
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                          ORIGINAL SOURCE:
ORGANISM: HTLV-III
                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                  FEATURE:
                                                                                                                                                                       HYPOTHETICAL:
                                                                                        NAME/KEY: Protein LOCATION: 1..512 OTHER INFORMATION:
                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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05-JUN-1995
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Gaps:
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160 471 140 360 100 300

180 531

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260 771 240 711 220 651 200 591

891 280

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RESULT 10
US-08-816-155B-45
; Sequence 45, Application US/08816155B
; Patent No. 5990091
; GENERAL INFORMATION:
; APPLICANT: TARTAGLIA, JAMES
; APPLICANT: GETTIG, RUSSELL R.
APPLICANT: MARTINEZ, HECTOR
; APPLICANT: MARTINEZ, HECTOR
; APPLICANT: PAOLETTI, ENZO
APPLICANT: PINCUS, STEVEN E.
; TITLE OF INVENTION: VECTORS HAVING ENHANCED EXPRESSION, AND
; TITLE OF INVENTION: METHODS OF MAKING AND USES THEREOF
; NUMBER OF SEQUENCES: 48
; CORRESSEE: FROMMER LAWRENCE & HAUG ILD
ADDRESSE: FROMMER LAWRENCE & HAUG LLP
STREET: 745 FIFTH AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10151
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/816,155B
FILING DATE: 12-MAR-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: KOWALSKI, THOMAS J.
REGISTRATION NUMBER: 32,147
REFERENCE/DOCKET NUMBER: 454310-2990
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-588-0800
TELEFAX: 212-588-0800
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Best Local Similarity:
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SEQUENCE CHARACTERISTICS:
LENGTH: 500 amino acids
TYPE: amino acid
STRANDEDNESS: n/a
TOPOLOGY: linear
MOLECULE TYPE: amino acid
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                                         CAGATGGTGCACCAGGCCATCAGCCCCCGCACCCTGAACGCCTGGGTGAAGGTGATCGAG
                                                                                           GCCGACGGC-----AAGGTGAGCCAGAACTACCCCCATCGTGCAGAACCTGCAGGGC
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Matches:
Conservative:
Mismatches:
Indels:
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RESULT 11
US-09-079-587-45
                                                                                                                                                                                                                                                                                        Sequence 45, Application US/09079587 Patent No. 6130066 GENERAL INFORMATION:
                                                                                                          APPLICANT: TARTAGLIA, JAMES
APPLICANT: COX, WILLIAM I.
APPLICANT: GETTIG, RUSSELL R.
APPLICANT: MARTINEZ, HECTOR
APPLICANT: PAOLETTI, ENZO
APPLICANT: PINCUS, STEVEN E.
TITLE OF INVENTION: VECTORS HAV
TITLE OF INVENTION: METHODS OF
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSE: FROMMER LAWRENCE &
GTBEET: 745 EIETH AVAILABLE
ZIP: 10151
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                 STATE: N
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                                                                  RESSEE: FROMMER LAWREN
JET: 745 FIFTH AVENUE
T: NEW YORK
TE: NEW YORK
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                                                   USA
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Best Local Similarity:
Query Match:
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STRANDEDNESS: n/a
TOPOLOGY: linear
MOLECULE TYPE: amino
US-09-079-587-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-475-704A-4 (1-1509) x US-09-079-587-45 (1-500)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Vel
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,587
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/816,155
FILING DATE: 12-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: KOWALSKI, THOMAS J.
REGISTRATION NUMBER: 32,147
REFERENCE/DOCKET NUMBER: 454310-2990
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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Conservative:
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RESULT 12
US-09-952-060-33
; Sequence 33, Application US,
; Patent No. 6733993
; GENERAL INFORMATION:
; APPLICANT: Emini, Emilio A
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APPLICANT: Bett, Andrew J.
APPLICANT: Chen, Ling
APPLICANT: Kaslow, David C.
APPLICANT: Shiver, John W.
APPLICANT: Shiver, John W.
APPLICANT: Toner, Timothy J.
APPLICANT: Casimiro, Danilo R.
TITLE OF INVENTION: ENHANCED FIRST GENERATION ADENOVIRUS
TITLE OF INVENTION: VACCINES EXCRESSING CODON OPTIMIZED HIV.
TITLE OF INVENTION: WODIFICATIONS
FILE REFERENCE: 20747Y
CURRENT APPLICATION NUMBER: US/09/952,060
CURRENT FILING DATE: 2001-09-14
PRIOR APPLICATION NUMBER: PCT/US01/28861
PRIOR FILING DATE: 2001-09-14
PRIOR APPLICATION NUMBER: FO/317,814
PRIOR APPLICATION NUMBER: 60/317,814
PRIOR APPLICATION NUMBER: 60/279,056
PRIOR APPLICATION NUMBER: 60/279,056
PRIOR APPLICATION NUMBER: 60/279,056
PRIOR APPLICATION NUMBER: 60/233,180
PRIOR APPLICATION NUMBER: 60/233
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Pred. No.:
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DB:
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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: tPA-gag fusion
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Conservative:
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Gaps:
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RESULT 13
US-08-127-499A-11
; Sequence 11, Application US/08127499A
; Patent No. 5510264
; GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS
TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES
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STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/127,499A
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/102/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5399
TELEYA. (202)672-5399
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
TYPE: amino acid
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TOPOLOGY: un
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Matches:
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; Patent No. 5556757
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TELEX: 904136
INFORMATION FOR SEQ ID NO: 11
SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 51916/104/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5399
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 20007-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,847
FILING DATE: 07-JUN-1995
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APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND
TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF
NUMBER OF SEQUENCES: 40
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ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              No . .
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CITY: Washington
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Matches:
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; TOPOLOGY: linear
; MOLECULE TYPE: pept
US-08-392-794A-2
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APPLICATION NUMBER: US 08/164
FILING DATE: 10-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: NEIMARK, SHERIDAN
REGISTRATION NUMBER: 20,520
REFERENCE/DOCKET NUMBER: HU=4/
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: HU, Yu-Wei
TITLE OF INVENTION:
TITLE OF INVENTION: J
NUMBER OF SEQUENCES:
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LENGTH: 437 amino acids
TYPE: amino acid
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version
CURRENT APPLICATION DATA:
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ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W.
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                                                                                                                  CTGCGCCCCGGCGGCAAGAAGCACTACATGCTGAAGCACCTGGTGTGGGCCAGCCGCGAG
                                                                                                                                                             MetGlyAlaArgAlaSerValLeuSerGlyGlyGluLeuAspArgTrpGluLysIleArg
 ATGAAGCAGCTGCAGCCCGCCCTGCAGACCCGCACCGAGGAGCTGCCAGCCTGTACAAC
                                                                                               LeuArgProGlyGlyLysLysLysTyrLysLeuLysHisIleValTrpAlaSerArgGlu
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                              LeuGluArgPheAlaValAsnProGlyLeuLeuGluThrSerGluGlyCysArgGlnIle
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Search completed: March 11, 2005, 15:46:26 Job time: 76.6742 secs

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Aae37600 HIV-1 sub
Adp02848 Wild type
Adp02847 Wild type
Aae18303 Human imm
Aam48948 HIV-1 sub
Adc72879 HIV-1 gag
Adc72880 HIV-1 gag
Adc72910 HIV-1 gag
Adn36406 Human pro
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## ALIGNMENTS

RESULT 1
AAY96944
ID AAY9 Human immunodeficiency virus; type C strain AF110967 Synthetic. 30-DEC-1999; Gag; expression cassette; antigenic; type C; HIV; Env; synthetic; DNA immunization; packaging cell line; antigen presentation. HIV synthetic Gag containing polypeptide. 31-OCT-2000 Barnett S, 31-DEC-1998; 01-SEP-1999; 06-JUL-2000. AAY96944; AAY96944 standard; WO200039304-A2 (CHIR ) CHIRON CORP. Zur Megede (first entry) 98US-0114495P. 99US-0152195P. 99WO-US031273 protein; 502 4 B

Polynucleotide encoding antigenic type C HIV Gag polypeptide or a HIV Env polypeptide and the polypeptide useful for immunizing a mammal especially human against HIV.

WPI; 2000-452401/39.

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y Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genes, useful infection.
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US-09-475-704A-4 (1-1509) x ADP02847
                                                                                                                                                                                                   The invention relates to a vector including a nucleotide sequence encoding an HIV Gag polypeptide, where the nucleotide sequence encoding the Gag polypeptide comprises a sequence having at least 90% sequence identity to 1549 (S1) or 1479 (S2) bp defined in the specification. The vector is useful as a vaccine for the treatment or prophylaxis of HIV infection in a mammal, where the vaccine induces an immunogenic response to the virus-like particles in a suitable susceptible host. This sequence corresponds to an HIV-1 gag protein sequence used in the method of the
                                                                                                                                                                                       corresponds invention.
                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                 New vector including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-DEC-2003;
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                                                                                                                           Olmsted F
Davis N,
                                                   Composition useful for treating or preventing HIV infections, two or more isolated nucleic acids encoding env, gag or pol g of HIV or immunogenic fragment of the gene products.
      The invention relates to encoding env, gag or pol
                                    Example
                                                                                                                                                                                     07-JUL-2000; 2000US-0216995P
                                                                                                                                                                                                        09-JUL-2001; 2001WO-US021701
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07-MAY-2002
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                                                                                                                                                                                                                                                                                   immunodeficiency virus; vaccine; HIV infection;
virus replicon; therapy; gag gene.
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Alignment Scores:
Pred. No.:
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Query Match:
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6.79e-131 2440.00 94.42% 92.43% 92.43% 85.92%

Length:
Matches:
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                                                 The invention relates to a novel method of determining whether a compound inhibits formation of a complex between HIV nucleocapsid protein 7 (NCp7) polypeptide and an HIV-psi-site oligonucleotide. The method involves adding the HIV-psi-site oligo to a mixture of the NCp7 polypeptide and the novel compound and comparing amount of complex formed, with that formed in the absence of the compound, where a decrease in the amount of complex formed in presence of the compound indicates that the compound inhibits complex formation. The method of the invention involves anti-HIV activity. The compounds identified are useful for treating a subject infected with human immunodeficiency virus (HIV) by administering the compound to the subject. This sequence represents an HIV-1 gag protein which contains an NCp sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Method of determining whether a compound inhibits formation of complex between HIV nucleocapsid protein 7 polypeptide and HIV psi-site oligonucleotide by comparing amount of complex formed in presence/abserof compound.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 2; SEQ ID NO 109; 105pp; English.
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The invention relates to a novel method of determining whether a inhibits formation of a complex between HIV nucleocapsid protein polypeptide and an HIV-psi-site oligonucleotide. The method invol

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Method of determining whether a compound inhibits formation of complex between HIV nucleocapsid protein 7 polypeptide and HIV psi-site oligonucleotide by comparing amount of complex formed in presence/absence of compound.
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                                                                                                                                                                                                                                                                                                                                      Method of determining whether a compound inhibits formation of complex between HIV nucleocapsid protein 7 polypeptide and HIV psi-site oligonucleotide by comparing amount of complex formed in presence/absence of compound.
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                                        The invention relates to a nucleic acid vector comprising at least one HIV sequence operably linked to a promoter and encoding a protein that does not assemble into viral particles. The nucleic acid vector is useful in immunizing a subject against HIV infection. This sequence corresponds to a peptide used in the invention.
                                                                                                                                                                                                                                     Huang
                                                                                                                                          Nucleic acid vector comprising at least one HIV sequence operably linked to a promoter and encoding a protein that does not assemble into viral particles, useful in immunizing a subject against HIV infection.
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N-PSDB; ADN36395.
                      Sequence
                                                                                                                         Disclosure;
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                                                   GCCCCCGGCCAGATGCGCGACCCCCCGCGGCACCAGCACCCTG
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Mismatches:
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Novel genomic nucleic acids of non-subtype B human immunodeficiency type 1 useful for detecting and treating AIDS comprises a specific nucleotide sequence.
                                                                                                                                           02-NOV-1998;
                                                                                                                                                                      25-OCT-1999;
                                                                                                                                                                                                   11-MAY-2000
                                                                                                                                                                                                                            WO200026416-A1
                                                                                                                                                                                                                                                                                                 HIV-1; human immunodeficiency virus; non-subtype B;
                                                                                                                                                                                                                                                                                                                            HIV-1 non-subtype B clone 96ZM751-3 gag protein
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20-APR-2001 (first en
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present in invention provides the protein and coding sequences for a number of human immunodeficiency virus (HIV) type 1 non-subtype B isolates. The sequences shown include the near full-length coding sequences from each isolate, and the env, pol, vif, vpr, vpu, gag, tat, rev and nef proteins. These can be used to detect the presence of HIV-1 in a sample and to produce antibodies against non-subtype B HIV-1 virus. These antibodies can be used in vaccines to prevent and treat HIV infection. (Updated on 12-SEP-2003 to standardise OS field)
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                         GCCCCCGGCCAGATGCGCGACCCCCCCGCGGCACATCGCCGGCGCCCACCAGCACCCTG
                                                                              TTCAGCCCCGAGGTGATCCCCCATGTTCACCGCCCTGAGCGAGGGGCGCCCCCCCAGGAC
 CAGGAGCAGATCGCCTGGATGACCAGCAACCCCCCCGTGCCCGTGGGCGACATCTACAAG
                                                                                                                                          LeuAsnThrMet
                                                                                                                                                                   CTGAACACGATGTTGAACACCGTGGGCGGCCACCAGGCCGCCATGCAGATGCTGAAGGAC
                                                                                                                                                                                              LeuAspLysIleGluGluGluGlnAsnLysSerGlnGlnLysIleGlnLysThrGluAla
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89.24%
84.65%
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Indels:
Gaps:
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Matches:
Conservative:
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nMetLeuLysAsp

600

180 540 160 480 140 420 120

100

300

360

240

60

90

180

120

80

40

780

240

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RESULT 14
AAB69275
ID AAB69
XX
AC AAB69
XX
DT 12-SE
DT 20-AP
XX
DE HIV-1
XX
HIV-1
KW Vif;
XX
OS Human
XX
PN WO200
           WO200026416-A1
                              Human immunodeficiency
                                                                               HIV-1 non-subtype B clone 96ZM651-8 gag protein.
                                                                                                      12-SEP-2003
20-APR-2001
                                                                                                                                     AAB69275;
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                                                 immunodeficiency virus;
t; rev; nef; vaccine.
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                                                          gag;
                                                          pol;
                                                          env; vpu;
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Novel genomic nucleic acids type 1 useful for detecting nucleotide sequence.
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41; Fig 14; 131pp; English.
                                                                                                                                  Shaw GM,
                                                                                                                                                                       RES
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                                              of non-subtype B human immunodeficiency virus and treating AIDS comprises a specific
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The present in invention provides the protein and coding sequences number of human immunodeficiency virus (HIV) type 1 non-subtype B isolates. The sequences shown include the near full-length coding sequences from each isolate, and the env, pol, vif, vpr, vpu, gag, rev and nef proteins. These can be used to detect the presence of H in a sample and to produce antibodies against non-subtype B HIV-1 v These antibodies can be used in vaccines to prevent and treat HIV infection. (Updated on 12-SEP-2003 to standardise OS field) virus. for a

494 AA;

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Percent Similarity:
Best Local Similarity:
Query Match:
 9.92e-129
2402.00
93.85%
90.28%
84.58%
Mismatches:
Indels:
Gaps:
                      Length:
Matches:
Conservative:
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12
12
12
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US-09-475-704A-4 (1-1509) x AAB69275 (1-494)

534	AAGGCCTTCAGCCCCGAGGTGATCCCCCATGTTCACCGCCCTGAGCGAGGGCGCCACCCCC :	475	8
160	MetValHisGlnLysLeuSerProArgThrLeuAsnAlaTrpValLysValIleGluGlu	141	DЬ
474	AGCCCCCGCACCCTGAACGCCTGGGTGAAGGTGATCGAGGAG	415	Ş
140	GlnAlaAlaAspGlyLysValSerGlnAsnTyrProIleValGlnAsnLeuGlnGlyGln	121	DВ
414	GCCGACGGCAAGGTGAAGCCAGAACTACCCCCATCGTGCAGAACCTGCAGGGCCAG	361	Ş
120	LeuAspArgIleGluGluGluGlnAsnLysIleGlnGlnLysIleGlnGlnLysThrGln	101	뮍
360	ATCGAGGAGGAGCAGAACAAGTCCCAGCAGAAGACCCAGCAGGCCAAGGAG	301	Ş
100	ThrValAlaThrLeuTyrCysValHisGluGlyValGluValArgAspThrLysGluAla 1	81	DЬ
300	GAGGTCCGCGACACCAAGGAGGCC	241	Ş
80	MetLysGlnLeuGlnProAlaLeuGlnThrGlyThrGluGluLeuArgSerLeuTyrAsn	61	망
240	ATGAAGCAGCTGCAGCCCGCCCTGCAGACCGGCACCGAGGAGCTGCGCAGCCTGTACAAC 2	181	Ş
60	LeuGluArgPheAlaLeuAsnProGlyLeuLeuGluThrSerGluGlyCysLysGlnIle	41	ఠ
180	CTGGAGGGCTTCGCCCTGAACCCCGGCCTGCTGGAGACCCGCCGAGGGCTGCAAGCAGATC	121	Ş
40	LeuArgProGlyGlyLysLysArgTyrMetIleLysHisLeuValTrpAlaSerArgGlu	21	ρģ
120	AAGCACCTGGTGTGGGCCAGCCGCGAG	61	8
20	MetGlyAlaArgAlaSerIleLeuArgGlyGlyLysLeuAspLysTrpGluLysIleArg	Д	망
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                CCCCTGAGCCAG
                                                                                                              GlyArgProGlyAsnPheLeuGlnAsnArgProGl
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                                                                          AAGGACCGCGAGCCCTACCGCGAGCCCCTGACCGCCCTGCGCCAGCCTGTTCGGCAGCGGC
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complex; HIV nucleocapsid protein 7; NCp7; HIV-psi-site; anti-HIV; human immunodeficiency virus; HIV.
10-JAN-2003; 2003WO-US000801
                                                                                                                                                                                                                                                                                                                ADC72875
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                                                                                                                            immunodeficiency virus 1.
                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                containing
                                                                                                                                                                                                                                  an NCp sequence,
                                                                                                                                                                                                                                  SEQ ID No
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WPI; 2003-646042/61. Beuchter D, 11-JAN-2002; 2002US-0347369P ACHILLION PHARM INC Hou X, Marlor CW, Rice WG, Yang

Method of determining whether a compound inhibits formation of complex between HIV nucleocapsid protein 7 polypeptide and HIV psi-site oligonucleotide by comparing amount of complex formed in presence/absence

Claim 2; SEQ ID NO 105; 105pp; English

The invention relates to a novel method of determining whether a compound inhibits formation of a complex between HIV nucleocapsid protein 7 (NCp7) polypeptide and an HIV-psi-site oligonucleotide. The method involves adding the HIV-psi-site oligo to a mixture of the NCp7 polypeptide and the novel compound and comparing amount of complex formed, with that formed in the absence of the compound, where a decrease in the amount of complex formed in presence of the compound indicates that the compound inhibits complex formation. The method of the invention involves anti-HIV activity. The compounds identified are useful for treating a subject infected with human immunodeficiency virus (HIV) by administering the compound to the subject. This sequence represents an HIV-1 gag protein which contains an NCp sequence of the invention.

Sequence 508 B

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CTGCGCCCCGGCGGCAAGAAGCACTACATGCTGAAGCACCTGGTGTGGGCCAGCCGCGAG
                               MetGlyAlaArgAlaSerIleLeuArgGlyThrLysLeuAspAlaTrpGluLysIleArg
                                                        ATGGGCGCCCGCGAGCATCCTGCGCGCGAGAAGCTGGACAAGTGGGAGAAGATCCGC
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RESULT 15 ADC72875 ID ADC72

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-DB=Uniprot_03 -QFMT=fastan -SUFFIX=n2p.rup -MINMATCH=0.1 -LOOPELE-0 -LOOPEXT=0
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-USER=US09475704_@CGN_1 1_614_@runat_10032005_140221_14821 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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## ALIGNMENTS

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"Molecular cloning and phylogenetic analysi virus type 1 subtype C: a set of 23 full-le Botswana.";
J. Virol. 73:4427-4432(1999).
EMBL; AF110967; AAD17071.1; -.
HSSP; P24736; 1NCP.
GO; GO:0019012; C:virion; IEA.
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0005198; F:structural molecule activ GO; GO:0016032; P:viral life cycle; IEA.
InterPro; IPR000721; Gag_p24.
InterPro; IPR010999; Retrovir_p17.
InterPro; IPR000971; Retrovir_p17.
InterPro; IPR0009916; Retrov capsid_C.
InterPro; IPR0008916; Retrov capsid_N.
InterPro; IPR001878; Znf_CCHC.
Pfam; PF00540; Gag_p17; I.
Pfam; PF00098; Zf-CCHC.
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Q9WF78;
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MEDLINE=99214383; PubMed=10196340;
Novitsky V.A., Montano M.A., McLane M.F.,
Foley B.T., Ndung'u T.P., Rahman M., Makh
Essex M.;
PRINTS; PR00939; C2HCZNFINGER. PRINTS; PR00234; HIV1MATRIX. SMART; SM00343; ZnF_C2HC; 2.
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Name=gag;
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AIDS; Core protein; Metal-binding; Polyprotein; SEQUENCE 502 AA; 55969 MW; B3ACF1F712A0C50F
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SEQUENCE FROM N.A.

van Harmelen J.H., Williamson C., K.
Abdool Karim S.S., McCutchan F.;
Submitted (JUN-2001) to the EMBL/Ger
EMBL; AY043175; AAL05325.1; -.
PIR; S49086; S49086.
HSSP; Q70622; 1HVN.
                                                                                                                                 SEQUENCE FROM N.A.

MEDLINE=2156558; PubMed=11709097; DOI
van Harmelen J., Williamson C., Kim B.
Abdool Karim S.S., McCutchan F.;

"Characterization of full-length HIV t
South Africa.";

AIDS Res. Hum. Retroviruses 17:1527-15
                                                                                                                                                                                                                                                              Q901X9
Q901X9;
Q901X9;
01-DEC-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
Gag protein.
Name=gag;
Human immunodeficiency v
Viruses; Retroid viruses
NCBI_TaxID=11676;
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viruses; Retroviridae;
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25,
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annotation update)
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GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0005198; F:structural molecule activity; IE
GO; GO:0016032; P:viral life cycle; IEA.
Pfam; PF00540; Gag_p17; 1.
Pfam; PF00607; Gag_p24; 1.
Pfam; PF00098; zf-CCHC; 2.
PRINTS; PR00939; C2HCZNFINGER.
PRINTS; PR00934; HIVIMATRIX.
SMART; SM00343; ZnF_C2HC; 2.
PROSITE; PS50158; ZF_CCHC; 2.
PROSITE; PS50158; ZF_CCHC; 2.
AIDS; Core protein; Metal-binding; Polyprotein; Zine SeQUENCE 492 AA; 55196 MW; CFDABOD5BA9F4BE9 CR
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O90056 PRELIMINARY; PRT; 500 I
O90056;
O1-NOV-1998 (TrEMBLrel. 08, Created)
O1-NOV-1998 (TrEMBLrel. 08, Last sequence
O1-OCT-2003 (TrEMBLrel. 25, Last annotatic
Gag protein.
Name=gag;
Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Le
NCBI_TaxID=11676;
[1]
SEQUENCE FROM N.A.
MEDLINE=99102570; PubMed=9847317;
Lole K.S., Bollinger R.C., Paranjape R.S., Gadkari D.,
Novak N.G., Ingersoll R., Sheppard H.W., Ray S.C.;
"Full-length human immunodeficiency virus type 1 genom
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Best Local Similarity:
Query Match:
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J. Virol. 73:152-160(1999).

REMBL; AF067154; AAD12071.1; -.

RHSSP; Q70622; 1HVN.

GO; GO:0019012; C:virion; IEA.

GO; GO:0003676; F:nucleic acid binding; IEA.

GO; GO:0005198; F:structural molecule activity; IEA.

GO; GO:0005198; F:structural molecule activity; IEA.

GO; GO:0005198; F:structural molecule activity; IEA.

RGO; GO:0016032; P:viral life cycle; IEA.

InterPro; IPR000721; Gag_p24.

InterPro; IPR000721; Retrovir_matrix.

InterPro; IPR0009916; Retrov_capsid_C.

InterPro; IPR008916; Retrov_capsid_N.

InterPro; IPR008919; Retrov_capsid_N.

InterPro; IPR001878; Znf CCHC.

R InterPro; IPR001878; Znf CCHC.

R Ffam; PF00540; Gag_p17; I.

Pfam; PF00540; Gag_p24; 1.

Pfam; PF00540; Gag_p24; 1.

Pfam; PF00593; zf-CCHC; 2.

PRINTS; PR00939; d2HCZNFINGER.

PRINTS; PR00934; HIVIMATRIX.

R PRINTS; PR00343; ZnF C2HC; 2.

PROSITE; PS50158; ZF CCHC; 2.

AIDS; Core protein; Metal-binding; Polyprotein; Zin

SEQUENCE 500 AA; 55878 MW; 25AA23024004E325 CRC
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R EMBL; AF544010; AAO16234.1; -.

R EMBL; AF544010; AAO16234.1; -.

R GO; GO:0019012; C:virion; IEA.

R GO; GO:0019012; C:virion; IEA.

R GO; GO:0005198; F:structural molecule activity;

R GO; GO:0016032; P:viral life cycle; IEA.

R GO; GO:0016032; P:viral life cycle; IEA.

R InterPro; IPR000721; Gag_p24.

R InterPro; IPR000916; Retrovir_p17.

R InterPro; IPR0008916; Retrov_capsid_C.

R InterPro; IPR0008916; Retrov_capsid_N.

R InterPro; IPR001878; Znf_CCHC.

R Pfam; PF00540; Gag_p24; 1.

Pfam; PF00607; Gag_p24; 1.

Pfam; PF00607; Gag_p24; 1.

R Pfam; PF000043; Znf_CCHC; 2.

R PROSITE; PS50158; ZF_CCHC; 2.

R AIDS; Core protein; FOlyprotein.
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Name=gag;
Nume=gag;
Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retrovi
K NCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                                               SEQUENCE
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 CACCAGGCCATCAGCCCCCGCACCCTGAACGCCTGGGTGAAGGTGATCGAGGAGAAGGCC
                AlaAspGlyLysValSerGlnAsnTyrProIleValGlnAsnLeuGlnGlyGlnMetVal
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R GO; GO:0019012; C:virion; IEA.

R GO; GO:0019012; C:virion; IEA.

R GO; GO:0003676; F:nucleic acid binding; IEA.

R GO; GO:0005198; F:structural molecule activity; IEA.

R GO; GO:0016032; P:viral life cycle; IEA.

R InterPro; IPR000721; Gag_p24.

R InterPro; IPR000071; Retrovir_matrix.

R InterPro; IPR0008916; Retrov_capsid_C.

R InterPro; IPR008919; Retrov_capsid_N.

InterPro; IPR001878; Znf_CCHC.

R InterPro; IPR001878; Znf_CCHC.

R InterPro; IPR001878; Znf_CCHC.

R Fam; PF00607; Gag_p24; 1.

R Pfam; PF00607; Gag_p24; 1.

R Pfam; PF00098; zf-CCHC; 2.

PRINTS; PR00939; C2HCZNFINGER.

PRINTS; PR0034; HIVIMATRIX.

RMART; SM00343; ZnF_CCHC; 2.

PROSITE; PS50158; ZF_CCHC; 2.

PROSITE; PS50158; ZF_CCHC; 2.

PROSITE; PS50158; ZF_CCHC; 2.

RAIDS; Core protein; Metal-binding; Polyprotein; Zir

SEQUENCE 495 AA; 55437 MW; 480D89863166ABCB CRC
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HSSP; P12493; 1AK4.
GO; GO:0019012; C:virion; IEA.
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0005198; F:structural mc1-
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PubMed=14686322; DOI=10.1089/088922203322588396;
Papathanasopoulos M.A., Patience T., Meyers T.M., McCutchan
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Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae;
NCBI_TaxID=11676;
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DE Gag protein.
GN Viruses; Retroid viruses;
OX NCBI_TAXID=11676;
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RA MARILIAMSON C., Ndung'u T.
RA Novitsky V.A., McLane M.F.
RA Novitsky V.A., McLane M.F.
RA Chang S.-Y., Peter T., Th.
RA MARILIAM R., Lee T.-H., Es
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NOVITSKY V.A., McLane M.F., Chigwedere P., Ndung'u Chang S.-Y., Peter T., Thior I., Rybak N., Gaseits:

A Marlink R., Lee T.-H., Essex M.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ datal
REMBL; AF443112; AAL34891.1; -.
RSP; P24736; INCP.
GO; GO:0019012; C:virion; IEA.
GO; GO:0015198; F:nucleic acid binding; IEA.
GO; GO:0015198; F:structural molecule activity; IEJ.
GO; GO:0016032; P:viral life cycle; IEA.
Pfam; PF00540; Gag_D17; 1.
Pfam; PF00607; Gag_D24; 1.
Pfam; PF00098; zf-CCHC; 2.
SMART; SM00343; ZnF_C2HC; 2.
ROSITE; PS50158; ZF_CCHC; 2.
AIDS; Core protein; Polyprotein.
SEQUENCE 499 AA; 55681 MW; OBFB37A38CA5779E CRC
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MEDLINE=21988475; PubMed=11991972;

DOI=10.1128/JVI.76.11.5435-5451.2002;

Novitsky V., Smith U.R., Gilbert P., McLane M.F., Chi Williamson C., Ndung'u T., Klein I., Chang S.-Y., Pet Foley B.T., Gaolekwe S., Rybak N., Gaseitsiwe S., Var Marlink R., Lee T.-H., Essex M.;

"Human immunodeficiency virus type 1 subtype C molecuconsensus sequence for an AIDS vaccine design?";

J. Virol. 76:5435-5451(2002).
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DE Gag protein.
GN Name=gag;
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DR Pfam; PF00540
consensus sequence for an AIDS vaccine design?";

J. Virol. 76:5435-5451(2002).

[2]

SEQUENCE FROM N.A.

Novitsky V.A., McLane M.F., Chigwedere P., Ndung's Chang S.-Y., Peter T., Thior I., Rybak N., Gaseit Marlink R., Lee T.-H., Essex M.;

Submitted (OCT-2001) to the EMBL/GenBank/DDBJ dat EMBL; AF443109; AAL34864.1; -.

SUBMITTED (OCT-2001) TO THE EMBL/GenBank/DDBJ dat EMBL; AF443109; AAL34864.1; -.

RMSP; P24736; 1NCP.

GO; GO:0019012; C:virion; IEA.

GO; GO:0003676; F:nucleic acid binding; IEA.

GO; GO:0005198; F:structural molecule activity; 1

GO; GO:0016032; P:viral life cycle; IEA.

Pfam; PF00540; Gag_D17; 1.

Pfam; PF0057; Gag_D24; 1.
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MEDLINE=21988475; PubMed=11991972;

DOI=10.1128/JVI.76.11.5435-5451.2002;

DOI=10.1128/JVI.76.11.5435-5451.2002;

Novitsky V., Smith U.R., Gilbert P., McLane M.F., Chigwedere P., Novitsky V., Smith U.R., Gilbert P., McLane M.F., Peter T., Thior I Foley B.T., Gaolekwe S., Rybak N., Gaseitsiwe S., Vannberg F., Foley B.T., Gaolekwe S., Rybak N., Gaseitsiwe S., Vannberg F., Marlink R., Lee T.-H., Essex M.;

"Human immunodeficiency virus type 1 subtype C molecular phylogeny: consensus sequence for an AIDS vaccine design?";

J. Virol. 76:5435-5451(2002).
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PRINTS; PR00939; C2HCZNFINGER.
PRINTS; PR00234; HIV1MATRIX.
SMART; SM00343; ZnF_C2HC; 2.
PROSITE; PS50158; ZF_CCHC; 2.
AIDS; Core protein; Metal-binding; Polyprotein; SEQUENCE 508 AA; 56799 MW; BFC5525AB8CAD688
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HIV HLA epitope mapping;
Korber B.T., Mullins J.I., Goulder P.J., Brander C
Moore S., Shindo N., Walker B.;
Submitted (NOV-2003) to the EMBL/GenBank/DDBJ data:
EMBL; AY463231; AAR27722.1; -.
HSSP; P12493; 1AFV.
GO; GO:0019012; C:virion; IEA.
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0005198; F:structural molecule activity; IE
GO; GO:0016032; P:viral life cycle; IEA.
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Q6S7X9;
Q5-JUL-2004 (TrEMBLrel.
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Name=gag;
Human immunodeficiency v
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R InterPro; IPR010999; Retrovir_matrix.
R InterPro; IPR000071; Retrovir_p17.
R InterPro; IPR0008916; Retrov_capsid_C.
R InterPro; IPR008919; Retrov_capsid_N.
InterPro; IPR001878; Znf_CCHC.
R InterPro; IPR001878; Znf_CCHC.
R Ffam; PF00540; Gag_p24; 1.
R Pfam; PF00607; Gag_p24; 1.
R Pfam; PF00607; Gag_p24; 1.
R Pfam; PF00098; zf-CCHC; 2.
R PRINTS; PR00939; C2HCZNFINGER.
R PRINTS; PR00934; HIVIMATRIX.
R SMART; SM00343; ZnF_CCHC; 2.
R PROSITE; PS50158; ZF_CCHC; 2.
SMART; Core protein; Metal-binding; Polyprotein; Zii SEQUENCE 497 AA; 55385 MW; 0CD9B58C540552BC CR
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AC Q90ME1;
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DT 01-DEC-2001 (TrEMBLrel. 1:
DT 01-DEC-2003 (TrEMBLrel. 2:
DE Gag protein.
GN Name=gag;
OS Human immunodeficiency vi:
OC Viruses; Retroid viruses;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21565559; PubMed=:
RA Engelbrecht S., de Villie
 SEQUENCE FROM N.A. MEDLINE=21565559; PubMed=11709098; DOI=10.1089/08892220152644241; Engelbrecht S., de Villiers T., Sampson C.C., zur Megede J.,
                                               Human immunodeficiency virus 1.
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T "Genetic analysis of the complete gag and env genes of

subtype C primary isolates from South Africa.";

L AIDS Res. Hum. Retroviruses 17:1533-1547(2001).

EMBL; AF391270; AAK77531.1; -.

R HSSP; P24736; 1NCP.

GO; GO:0019012; C:virion; IEA.

GO; GO:0003676; F:nucleic acid binding; IEA.

GO; GO:0005198; F:structural molecule activity; IEA.

R GO; GO:0016032; P:viral life cycle; IEA.

R GO; GO:0016032; P:viral life cycle; IEA.

R GO; GO:0016032; P:viral life cycle; IEA.

R Pfam; PF00540; Gag_p17; 1.

R Pfam; PF00540; Gag_p24; 1.

R Pfam; PF00598; zf-CCHC; 2.

R PFINTS; PR00939; C2HCZNFINGER.

R PRINTS; PR00934; HIVIMATRIX.

R PRINTS; PR00343; ZnF_C2HC; 2.

R PROSITE; PS50158; ZF_CCHC; 2.

AIDS; Core protein; Metal-binding; Polyprotein; Zinc; Z

SEQUENCE 492 AA; 54999 MW; B74F6064D506635D CRC64;
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Zinc; CRC64;

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Q9QN98 PRELIMINARY; PRT; 491 AA.
Q9QN98;
C Q9QN98;
C 01-MAY-2000 (TrEMBLrel. 13, Created)
C 01-MAY-2000 (TrEMBLrel. 25, Last sequence update)
C 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Gag.
Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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RA McChizuki N., Otsuka N., Matsuc K., Shiino T., Kojuma A., Kurata T.
RA Sakai K., Yamamoto N., Isomura S., Dhole T.N., Takebe Y., Matsuda M.
RA Tatsumi M.;
RA McChizuki M.;
RA McChilling M.;
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RA 
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HisGlnAlaIleSerProArgThrLeuAsnAlaTrpValLysValIleGluGluLysAla
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A Abdool Karim S.S., McCutchan F.;
A bdool Karim S.S., McCutchan F.;
A memble Addool Karim S.S., McCutchan F.;
A colonical C. virion; IEA.
B GO; GO:0019012; C:virion; IEA.
B GO; GO:0005198; F:structural molecule activity; IE;
B GO; GO:0016032; P:viral life cycle; IEA.
B GO; GO:0016032; P:viral life cycle; IEA.
B GO; GO:0016032; P:viral life cycle; IEA.
B Ffam; PF00540; Gag_p17; 1.
B Pfam; PF00540; Gag_p24; 1.
B Pfam; PF00540; Gag_p24; 1.
B Pfam; PF00698; zf-CCHC; 2.
B PRINTS; PR00939; C2HCZNFINGER.
B PRINTS; PR00934; HIVIMATRIX.
B PRINTS; PR00934; ZF-CCHC; 2.
B PROSITE; PS50158; ZF-CCHC; 2.
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MEDLINE=21565558; PubMed=11709097; DOI=10.1089/08892220152644232;
van Harmelen J., Williamson C., Kim B., Morris L., Carr J.,
Abdool Karim S.S., McCutchan F.;
"Characterization of full-length HIV type 1 subtype C sequences fisouth Africa.";
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AIDS Res. Hum. Retroviruses 17:1527-1531(2001).
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A Gupta R.M., Prasad V., Singh B., Seth P.;

A Gupta R.M., Prasad V., Singh B., Seth P.;

B Submitted (JUL-2002) to the EMBL/GenBank/DDBJ data

R EMBL; AF533131; AAP87971.1; -.

R GO; GO:0019012; C:virion; IEA.

GO; GO:0003676; F:nucleic acid binding; IEA.

GO; GO:0005198; F:structural molecule activity; IE,

GO; GO:0016032; P:viral life cycle; IEA.

GO; GO:0016032; P:viral life cycle; IEA.

InterPro; IPR000721; Gag_p24.

InterPro; IPR00099; Retrovir_matrix.

InterPro; IPR000916; Retrovir_D17.

InterPro; IPR000916; Retrov capsid_C.

R InterPro; IPR0008916; Retrov capsid_N.

R InterPro; IPR0008916; Retrov capsid_N.

R InterPro; IPR001878; Znf_CCHC.

R Ffam; PF00540; Gag_p17; I.

R Pfam; PF00540; Gag_p17; I.

R Pfam; PF00098; zf-CCHC; 2.

R Pfam; PF00098; zf-CCHC; 2.

R PART; SM00343; ZnF_C2HC; 2.

R PROSITE; PS50158; ZF_CCHC; 2.

A R POSITE; PS50158; ZF_CCHC; 2.

SAART; Core protein; Folyprotein.
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Viruses; Retroid viruses; Retroviridae;
NCBI TaxID=11676;
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A Abdool Karim S.S., McCutchan F.;

L Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.

R EMBL; AY043173; AAL05307.1; -.

R EMBL; AY043173; AAL05307.1; -.

R GO; GO:0019012; C:virion; IEA.

GO; GO:0005198; F:nucleic acid binding; IEA.

GO; GO:0005198; F:structural molecule activity; IEA.

GO; GO:0005198; F:structural molecule activity; IEA.

R GO; GO:0016032; P:viral life cycle; IEA.

R GO; GO:0016032; P:viral life cycle; IEA.

R Pfam; PF00540; Gag_p17; 1.

R Pfam; PF00540; Gag_p24; 1.

R Pfam; PF005098; zf-CCHC; 2.

R SMART; SM00343; ZnF C2HC; 2.

R PROSITE; PS50158; ZF CCHC; 2.

R ALDS; Core protein; Folyprotein.

SEQUENCE 492 AA; 55205 MW; 55CE9EE2D591BA3A CRC64;
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Viruses; Retroid viruses; Retroviridae;
NCBI_TaxID=11676;
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                          CysArgAlaProArgLysLysGlyCysTrpLysCysGlyLysGluGlyHisGlnMetLys
                                  TGCCGCGCCCCCCGCAAGAAGGGCTGCTGGAAGTGCGGCAAGGAGGGCCACCAGATGAAG
                                                          GGCCCCCGGCGCAACGTCAAGTGCTTCAACTGCGGCAAGGAGGGCCCACATCGCCAAGAAC
                                                                                                     GCCGAGGCGATGAGCCAGGCCAACAGCGTGAACATCATGATGCAGAAGAGCAACTTCAAG
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RP SEQUE
RX MEDLI
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RX MEDLINE=21565559; PubMed=11709098; DOI=10.1089/08892220152644241;

RA Engelbrecht S., de Villiers T., Sampson C.C., zur Megede J.,

RA Engelbrecht S.W., van Rensburg E.J.;

RT "Genetic analysis of the complete gag and env genes of HIV type 1

RT subtype C primary isolates from South Africa.";

RI AIDS Res. Hum. Retroviruses 17:1533-1547(2001).

DR HIDS RES. Hum. Retroviruses 17:1533-1547(2001).

DR HSSP; P24736; 1NCP.

DR HSSP; P24736; 1NCP.

DR GO; GO:0019012; C:virion; IEA.

GO; GO:0019012; C:virion; IEA.

GO; GO:0005198; F:structural molecule activity; IEA.

DR GO; GO:0005198; F:structural molecule activity; IEA.

DR GO; GO:0016032; P:viral life cycle; IEA.

DR Pfam; PF00540; Gag_p17; 1.

Pfam; PF00098; zf-CCHC; 2.

PROSITE; PS50158; ZF CCHC; 2.

PROSITE; PS50158; ZF CCHC; 2.

RADS; Core protein; Polyprotein.

SQ SEQUENCE 492 AA; 55186 MW; E8023DE89216F43D CRC64;
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Search completed: March 11, 2005, 15:39:49 Job time : 289.58 secs

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Adm73759 HIV-1 pol
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Adm73763 HIV-1 pol
Aaa51626 HIV codon
Aal44553 HIV-1 p55
Abl39972 Synthetic
Adm73785 HIV-1 pol
Abl40020 Synthetic
Adm73833 HIV-1 pol
Aaa51609 HIV synth
Aal44548 HIV-1 p55
Abl39953 Synthetic
Adm73758 HIV-1 pol
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Adc13237 DNA of HI
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## ALIGNMENTS

RESULT 1
AAA51610
ID AAA5 30-DEC-1999; HIV synthetic Gag polynucleotide. WO200039304-A2 Human immunodeficiency virus; type C strain AF110967. Gag; expression cassette; antigenic; type C; HIV; Env; synthetic; DNA immunization; packaging cell line; antigen presentation; ss. 31-OCT-2000 (first entry) AAA51610 standard; DNA; 1509 99WO-US031273. BP.

Barnett S, 31-DEC-1998; 01-SEP-1999; (CHIR ) CHIRON CORP. Zur Megede 98US-0114495P. 99US-0152195P. ū

Polynucleotide encoding antigenic type polypeptide and the polypeptide useful human against HIV. C HIV Gag polypeptide or for immunizing a mammal e especially

WPI; 2000-452401/39.

Claim 2; Page 93; 113pp; English.

Expression cassettes comprising a polynucleotide encoding antigenic typ C human immunodeficiency virus (HIV) Gag or Env polypeptides are useful in DNA immunization, generation of packaging cell lines and production Gag- and/or Env-containing proteins. Synthetic Env and Gag expression cassettes exhibit increased potency for induction of cytotoxic T-lymphocyte (CTL) responses by DNA immunization. Gag of HIV-1 selftype of

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Matches 1509;
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                                                                                28-SEP-2000; 2000US-0236105P.
30-AUG-2001; 2001US-0315905P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A microparticle to which a biologically active macromolecule is adsorbed, for use as a vaccine composition to treat viral, bacterial or parasitic infections, comprises a polymer microparticle, a detergent and a
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Human immunodeficiency virus type C; immunogenic; immunisation; gag; pol;
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standard; DNA; 1509

Gag

polynucleotide sequence

SEQ ID

NO:4.

antigenic HIV type C vif; vpr; tat; rev; v

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Best Local Similarity
Matches 1509; Conserv
                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an expression cassette comprising a polynucleotide sequence encoding an HIV Pol polypeptide. The invention also relates to a recombinant expression system for use in a host cell comprising an expression cassette, where the polynucleotide sequence further comprises control elements capable of driving expression in the selected host cell, a cell comprising an expression cassette where the polynucleotide sequence further comprises control elements compatible with the expression in the cell and a composition for generating an immunological response, comprising an expression cassette. The expression cassette and the methods of the invention are useful in eliciting an immune response, in DNA immunisation, in generation of packaging cell lines and in producing HIV Type C proteins. This sequence represents an HIV-1 polynucleotide of the invention.
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                                                                          The present invention describes expression cassettes comprising a polynucleotide sequence encoding a polypeptide comprising immunogenic HIV type C polypeptides. The expression cassettes comprise any of the HIV type C sequences encoding Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env or Nef (I). (I) have immunostimulant activity and can be used in gene therapy. The HIV type C polynucleotides are useful in applications including DNA immunisation, generation of packaging cell lines, and production of HIV Type C proteins. The polynucleotides are particularly useful in gene therapy and DNA immunisation applications. ABL39942 to ABL40054 and ABB06204 to ABB06215 represent sequences used in the exemplification of
                                                                                                                                                                                                                                                                                                                                         New polynucleotides encoding antigenic HIV applications including DNA immunization or lines, particularly in gene therapy.
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 GAGGAGATGATGACCGCCTGCCAGGGCGTGGGCCGCCGGCCACAAGGCCCGCGTGCTG
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                                                                          CAGAACGCCAACCCCGACTGCAAGACCATCCTGCGCGCTCTCGGCCCCGGCGCCACCCTG
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AC ADM7
AC ADM7
AC ADM7
XX
DT 03-J
XX
HIV-
KW HIV-
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                      New expression cassette comprising a polynucleotide sequence encoding an HIV Pol polypeptide, useful in eliciting an immune response, in DNA immunization, generating of packaging cell lines or in producing HIV Type
                                                                                                                                                                                                                                           04-DEC
                                                                                                                                                                                                                                                                                            Human immunodeficiency virus 1.
                                                                                                                                                                                                                                                                                                                   HIV-1; gene; ds; HIV pol; immune response; DNA immunisation; HIV type C protein; immunostimulant.
                                                                                                                                                                                                                                                                                                                                                          HIV-1 polynucleotide
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                                                                                                                                                                                                                                                                                                                                                                                                            ADM73763;
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                                                                            WPI; 2004-060515/06.
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                                                                                                                            (MEGE/)
(BARN/)
(ENGE/)
(RENS/)
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) BARNETT S W.
) ENGELBRECHT S.
) RENSBURG E J V.
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Example 1; SEQ ID NO 21; 160pp; English
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The invention relates to an expression cassette comprising a polynucleotide sequence encoding an HIV Pol polypeptide. The invention also relates to a recombinant expression system for use in a host cell comprising an expression cassette, where the polynucleotide sequence further comprises control elements capable of driving expression in the selected host cell, a cell comprising an expression cassette where the polynucleotide sequence further comprises control elements compatible with the expression in the cell and a composition for generating an immunological response, comprising an expression cassette. The expression cassette and the methods of the invention are useful in eliciting an immune response, in DNA immunisation, in generation of packaging cell lines and in producing HIV Type C proteins. This sequence represents an HIV-1 polynucleotide of the invention.

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Sequence
     1509 BP;
321 A; 560 C; 470 G; 158
     T; 0 U;
      0 Other;
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Query Match Best Local Similarity Matches 1498; Conserv 98.8%; ilarity 99.3%; Conservative <u>.</u> Score 1491.4; Pred. No. 7.7e 0; Mismatches 4; DB 12; 7.7e-175; 1eB 11; II Indels Length 1509; 0; Gaps

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Matches 1497; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1509 BP; 321 A; 559 C; 471 G; 158 T; 0 U; 0 Other;
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HIV; ds; vaccine; gene; immune response; microparticle; adsorbent surface; poly(alpha-hydroxy acid); polyhydroxy butyric acid; polycaprolactone; polyorthoester; polycyanoacrylate; detergent; submicron emulsion; viral infection; bacterial infection; parasitic infection; HIV-1 p55gag polypeptide.

p55gag polypeptide coding sequence

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(CHIR CHIRON CORP.

O'hagan I Ulmer J, 1 D, Occ. J, Dubensky ' Otten G, hubensky TW; Donnelly 'n, Polo , M Barnett S Singh

WPI; 2002-519084/55.

A microparticle to which a biologically active macromolecule is adsorbed, for use as a vaccine composition to treat viral, bacterial or parasitic infections, comprises a polymer microparticle, a detergent and a emulsion.

Claim 72; Fig 6; 100pp; English.

The invention relates to a method of raising an immune response in a host animal. The method of the invention comprises administering a microparticle that has an adsorbent surface to which a first biologically active macromolecule (e.g. a nucleic acid) has been adsorbed. The microparticle comprises a polymer microparticle of poly(alpha-hydroxy acid), a polyhydroxy butyric acid, a polycaprolactone, a polycrthoester, a polycyanoacrylate, a detergent, and submicron emulsion. The method/microparticle of the invention is useful for immunising a host animal against viral, bacterial or parasitic infections. The present DNA sequence encodes a HIV-1 p55gag polypeptide. (Updated on 29-AUG-2003 to standardise OS field)

RESULT 8
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Matches 1497; Conserv
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                                                WPI; 2002-154920/20.
                                                                       Zur Megede J,
                                                                                                                                   05-JUL-2000; 2000US-00610313
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New polynucleotides encoding antigenic HIV Type C polypeptides, useful in applications including DNA immunization or generation of packaging cell lines, particularly in gene therapy.

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Matches 1402;
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                                                                                            HIV-1; gene; ds; HIV pol; immune response; DNA immunisation; HIV type C protein; immunostimulant.
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05-JUL-2001; 2001US-00899575
                                                                       Human immunodeficiency
                                                                                                                               HIV-1 polynucleotide
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Matches 1402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1494 BP; 325 A; 557 C; 455 G; 157 T; 0 U; 0 Other;
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) BARNETT S W.
) ENGELBRECHT S.
) RENSBURG E J V.
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                                                                       Query Match
Best Local
                                                   Matches 1401;
                                                                                                                                                           The invention relates to an expression cassette comprising a polynucleotide sequence encoding an HIV Pol polypeptide. The invention also relates to a recombinant expression system for use in a host cell comprising an expression cassette, where the polynucleotide sequence further comprises control elements capable of driving expression in the selected host cell, a cell comprising an expression cassette where the polynucleotide sequence further comprises control elements compatible with the expression in the cell and a composition for generating an immunological response, comprising an expression cassette. The expression cassette and the methods of the invention are useful in eliciting an immune response, in DNA immunisation, in generation of packaging cell lines and in producing HIV Type C proteins. This sequence represents an HIV-1 polynucleotide of the invention.
                                                                                                                                 Sequence 1491 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 8;
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                                                                       Similarity
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Polynucleotide encoding antigenic type C HIV Gag polypeptide or a HIV Env polypeptide and the polypeptide useful for immunizing a mammal especially
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Best Local Sim:
Matches 1399;
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Expression cassettes comprising a polynucleotide encoding antigenic type C human immunodeficiency virus (HIV) Gag or Env polypeptides are useful in DNA immunization, generation of packaging cell lines and production of Gag- and/or Env-containing proteins. Synthetic Env and Gag expression cassettes exhibit increased potency for induction of cytotoxic T-lymphocyte (CTL) responses by DNA immunization. Gag of HIV-1 self-assemble into non-infectious virus-like particles which are used as a matrix for the proper presentation of an antigen entrapped or associated to the immune system of the host
Sequence 1479 BP; 325 A; 529 C; 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human against
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G; 162
T; 0 U; 0 Other;
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Local Similarity

84.6%; 92.5%;

Score 1276.8; Pred. No. 1.7e 0; Mismatches

.7e-148; les 77;

Indels Length

DB 3;

Conservative

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778 721 601 481 478 421 418 361 361 301 301 241 241 181 181 121 121 62 61 CTGCAGGAGCAGATCGCCTGGATGACCAGCAACCCCCCCGTGCCCGTGGGCGACATCTAC GTGGCCCCGGCCAGATGCGCGACCCCCCGCGGCACATCGCCGGCGCCACCACCACCA GTGCACCAGGCCATCAGCCCCCGCACCCTGAACGCCTGGGTGAAGGTGATCGAGGAGAAG GCCGAC---GGCAAGGTGAGCCAGAACTACCCCCATCGTGCAGAACCTGCAGGGCCAGATG CTGGACAAGATCGAGGAGGAGGAGAACAAGTCCCCAGCAGAAGACCCCAGCAGGCCAAGGAG AAGCGGTGGATCATCCTGGGCCTGAACAAGATCGTGCGGATGTACAGCCCCGTGAGCATC GACCTGAACACGATGTTGAACACCGTGGGCGGCCACCAGGCCGCCATGCAGATGCTGAAG GACCTGAACACGATGTTGAACACCGTGGGCGGCCACCAGGCCGCCATGCAGATGCTGAAG GCCTTCAGCCCCGAGGTGATCCCCATGTTCACCGCCCTGAGCGAGGGGGCGCCACCCCCAG GTGCACCAGGCCATCAGCCCCCGCACCCTGAACGCCTGGGTGAAGGTGATCGAGGAGAAG GCCGACAAGGGCAAGGTGAGCCAGAACTACCCCATCGTGCAGAACCTGCAGGGCCAGATG CTGGACAAGATCGAGGAGGAGCAGAACAAGTGCCAGCAGAAGATCCAGCAGGCCGAGGCC **ACCGTGGCCACCCTGTACTGCGTGCACGAGGAGGTCCGAGGTCCGAGGACACCAAGGAGGCC** ACCGTGGCCACCCTGTACTGCGTGCACGCCCGCGATCGAGGTCCGCGAACACCAAGGAGGCC ATCCGCCAGCTGCACCCCGCCCTGCAGACCGGCAGCGAGGAGCTGAAGAGCCTGTTCAAC ATGAAGCAGCTGCAGCCCGCCCTGCAGACCGGCACCGAGGAGCTGCGCCAGCCTGTACAAC CTGGAGGGCTTCGCCCTGAACCCCGGCCTGCTGGAGACCGCCGAGGGCTGCAAGCAGATC CTGCGCCCCGGCGCAAGAAGCACTACATGCTGAAGCACCTGGTGTGGGCCCAGCCGCGAG ATGGGCGCCCGCGCATCCTGCGCGCGAGAAGCTGGACAAGTGGGAGAGATCCGC crecada a grince de crecada de consecuencia de la consecuencia della dell 837 657 597 537 477 417 300 777 720 660 600 540 480 420 360 360 300 240 240 180 120 120 780 60

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                                                            HIV; ds; vaccine; gene; immune response; microparticle; adsorbent surface; poly(alpha-hydroxy acid); polyhydroxy butyric polycaprolactone; polyorthoester; polycyanoacrylate; detergent; submicron emulsion; viral infection; bacterial infection; parasitic infection; HIV-1 p55gag polypeptide.
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08-NOV-2002
              WO200226209-A2
                                     Human immunodeficiency
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Query Match
Best Local Similarity
                                                                     The invention relates to a method of raising an immune response in a host animal. The method of the invention comprises administering a microparticle that has an adsorbent surface to which a first biologically active macromolecule (e.g. a nucleic acid) has been adsorbed. The microparticle comprises a polymer microparticle of poly(alpha-hydroxy acid), a polyhydroxy butyric acid, a polycaprolactone, a polyorthoester, a polycyanoacrylate, a detergent, and submicron emulsion. The method/microparticle of the invention is useful for immunising a host animal against viral, bacterial or parasitic infections. The present DNA sequence encodes a HIV-1 p55gag polypeptide. (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                 O'hagan D
Ulmer J,
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30-AUG-2001; 2001US-0315905P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 1399; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes expression cassettes comprising a polynucleotide sequence encoding a polypeptide comprising immunogenic HI type C polypeptides. The expression cassettes comprise any of the HIV type C sequences encoding Gag, Pol, Vif, Vpr, Tat, Rev, Vpu, Env or Nef (I). (I) have immunostimulant activity and can be used in gene therapy. The HIV type C polynucleotides are useful in applications including DNA immunisation, generation of packaging cell lines, and production of HIV Type C proteins. The polynucleotides are particularly useful in gene therapy and DNA immunisation applications. ABL39942 to ABL40054 and ABB06204 to ABB06215 represent sequences used in the exemplification of the polynucleotides are particularly useful in gene therapy and DNA immunisation applications. ABL39942 to ABL40054 and ABB06204 to ABB06215 represent sequences used in the exemplification of the polynucleotides are particularly useful in gene therapy and DNA immunisation applications. ABL39942 to ABL40054 and ABB06204 to ABB06215 represent sequences used in the exemplification of the polynucleotides are particularly useful in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New polynucleotides encoding antigenic HIV Type C polypeptides, useful applications including DNA immunization or generation of packaging cell lines, particularly in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human immunodeficiency virus type C; antigenic HIV type C protein; immunogenic; immunisation; gag; pol; vif; vpr; tat; rev; vpu; env; nef; immunostimulant; gene therapy; gene; ds.
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                    ACCGTGGCCACCCTGTACTGCGTGCACGCCGGCATCGAGGTCCGCGACACACCAAGGAGGCC
                                                                                            ATGAAGCAGCTGCAGCCCGCCCTGCAGAACCGGCACCGAGGAGCTGCGCAGCCTGTACAAC
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Search completed: March 12, 2005, 17:35:57 Job time: 862.019 secs

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Result
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Maximum DB
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AR373320 Sequence
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## ALIGNMENTS

REFERENCE AUTHORS TITLE RESULT 1
AX455888
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE 멍 8 g ঠ Query Match 100.0%; Score 1509; DB 6; Length 1509; Best Local Similarity 100.0%; Pred. No. 3.2e-150; Matches 1509; Conservative 0; Mismatches 0; Indels 0; JOURNAL ORGANISM 181 121 121 61 13 zur Megede, J., Barnett, S.W., Engelbrecht, S. and van Rensburg, E. Polynucleotides encoding antigenic hiv type c polypeptides, polypeptides and uses thereof Patent: WO 0204493-A 4 17-JAN-2002; CHIRON CORPORATION (US); University of Stellenbosch (ZA) Location/Qualifiers AX455888 1509 bp Sequence 4 from Patent WO0204493. AX455888 synthetic construct synthetic construct other sequences; artificial sequences. CTGGAGGGCTTCGCCCTGAACCCCGGCCTGCTGGAGACCGCCGAGGGGCTGCAAGCAGATC 180 ATGGGCGCCCGCGCCAGCATCCTGCGCGCGGCGAGAAGCTGGACAAGTGGGAGAAGATCCGC ATGAAGCAGCTGCAGCCCGCCCTGCAGACCGGCACCGAGGAGCTGCGCAGCCTGTACAAC CTGCGCCCCGGCGCAAGAAGCACTACATGCTGAAGCACCTGGTGTGGGCCCAGCCGCGAG CTGGAGGGCTTCGCCCTGAACCCCGGCCTGCTGGAGACCGCCGAGGGCTGCAAGCAGATC CTGCGCCCCGGCGGCAAGAAGCACTACATGCTGAAGCACCTGGTGTGGGCCAGCCGCGAG ATGGGCGCCCGCGCAGCATCCTGCGCGGCGAGAAGCTGGACAAGTGGGAAGAAGATCCGC /organism="synthetic construct"
/mol\_type="unassigned DNA"
/db\_xref="taxon:32630"
/note="synthetic Gag of HIV strain AF110967" DNA linear PAT 06-JUL-2002 0; Gaps 180 240 120 120 60

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GCCGACGGCAAGGTGAGCCAGAACTACCCCATCGTGCAGAACCTGCAGGGCCAGATGGTG
                                            CTGGACAAGATCGAGGAGGAGCAGAACAAGTCCCAGCAGAAGACCCCAGCAGGACCAAGGAG
                                                         CTGGACAAGATCGAGGAGGAGCAGAACAAGTCCCAGCAGAAGACCCCAGCAGGCCAAGGAG
                                                                                          ACCGTGGCCACCCTGTACTGCGTGCACGCCGGCATCGAGGTCCGCGACACCAAGGAGGCC
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/mol_type="unassigned DNA"
/db_xref="taxon:11676"
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/db_xref="taxon:32630"
/note="synthetic Gag coding seq
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D; Mismatches 12;
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RESULT 5 AX455935 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL FEATURES 90urce	Q Y	Q	₽ <b>Q</b>	B & B &	gg Qy	g &	р <i>Q</i>	д <i>Q</i> у	g Q	g s	B 84
AX455935  AX455935  AX455935  ON AX455935  AX455935  AX455935.1 GI:21714919  S  S synthetic construct other sequences; artificial sequences.  CE 1  RS zur Megede, J., Barnett, S.W., Engelbrecht, S. and van Rensburg, E. Polynucleotides encoding antigenic hiv type c polypeptides, polypeptides and uses thereof Patent: WO 0204493-A 51 17-JAN-2002; CHIRON CORPORATION (US); University of Stellenbosch (ZA)  CHIRON CORPORATION (US); University of Stellenbosch (ZA)	െ — െ	381 CCCGCCGAGAGCTTCCGCTTCGAGGAGACCACCCCCGCCCCCAAGCAGGAGCCCAAGGAC 144	321 CCCGGCAACTTCCTGCAGAACCGCAGCGAGCCGCCGCCCCCCCC	1201 TGCCGCGCCCCCGCAAGAAGGGCTGCTGGAAGTGCCGGCAAGGAGGACCACCAGATGAAG 1260	41 GGCCCCCGGCGCAACGTCAAGTGCTTCAACTGCGGCAAGGAGGGCCACATCGCCAAGAAC 12 	1081 GCCGAGGCGATGAGCCAAGGCCAACAGCGTGAACATCATGATGCAGAAGAGCAACTTCAAG 1140 	1021 GAGGAGATGATGACCGCCTGCCAGGGCGTGGGCGGCCCCGGCCACAAGGCCCGCGTGCTG 1080	961 CAGAACGCCAACCCCGACTGCAAGACCATCCTGCGCGCGC	901 CTGCGCGCGAGCAGGCCACCCAGGACGTGAAGAACTGGATGACCGAGACCCTGCTGGTG 960 	841 GACATCCGCCAGGGCCCCAAGGAGCCCTTCCGCGACTACGTGGACCGCTTCTTCAAGACC 900 	781 CGGTGGATCATCCTGGGCCTGAACAAGATCGTGCGGATGTACAGCCCCGTGAGCATCCTG 840 
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\$	g Qy	Query Ma Best Loc Matches	ORIGIN	FEATURES sourc	AUTHORS TITLE JOURNAL	SOURCE ORGANISM REFERENCE	DEFINITION ACCESSION VERSION KEYWORDS	RESULT 6 AX455983 LOCUS	D &	dy VQ	Qy Db	QV dd	Db QQ	gg Qy	dg VQ	Db Qy	B 8	DЬ
ш	1 ATGGGCGCCCGCGCCAGCATCCTGCGCGGCGAGAAGCTGGACAAGTGGGAGAAGATCCGC 60 	Match 85.8%; Score 1294.8; DB 6; Length 1491; Jocal Similarity 92.7%; Pred. No. 1.2e-127; 18 1401; Conservative 0; Mismatches 87; Indels 24; Gaps 3;	/mol_type="unassigned DNA"  /db_xref="taxon:32630"  /note="Gag_TV2_C_ZAopt"	^		<pre>synthetic construct  M synthetic construct  other sequences; artificial sequences.  1</pre>	Sequence 99 from Patent WO0204493. AX455983 AX455983.1 GI:21714967	AX455983	1498 CTGAGCCAGTAA 1509            1483 CTGAGCCAGTAA 1494	1438 GACCGCGAGCCCTACCGCGAGCCCCTGACCGCCCTGCGCAGCCTGTTCGGCAGCGGCCCC 1497	1378 CCCCCGCGAGAGCTTCCGCTTCGAGGAGACCACCCCCGCCCCCAAGCAGGAGCCCAAG 1437	1321 CCCGGCAACTTCCTGCAGAACCGCAGCGAGCCCCGCCGCCCCCACCGTGCCCACCGCC 1377	1261 GACTGCACCGAGCGCCAGGCCAACTTCCTGGGCAAGATCTGGCCCAGCCACAAGGGCCGC 1320	1201 TGCCGCGCCCCCGCAAGAAGGGCTGCTGGAAGTGCGGCAAGGAGGGCCACCAGATGAAG 1260 	1141 GGCCCCCGGCGAACGTCAAGTGCTTCAACTGCGGCAAGGAGGGGCCACATCGCCAAGAAC 1200 	1081 GCCGAGGCGATGAGCCAGGCCAACAGCGTGAACATCATGATGCAGAAGAGCAACTTCAAG 1140	1021 GAGGAGATGATGACCGCCTGCCAGGGCGTGGGCGGCCCCGGCCAAGGCCCGCGTGCTG 1080	
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1141 GGCCCCCGGCGCAACGTCAAGTGCTTCAACTGCGGCAAGGAGGGGCCACATCGCCAAGAAC 1200	1081 GCCGAGGCGATGAGCCAGGCCAACAGCGTGAACATCATGATGCAGAAGAGCGAACTTCAAG 1140	1 GAGGAGATGATGACCGCCTGCCAGGGCGTGGGCGGCCGCCCCGGCCACAAGGCCCGCGTGCTG 1	961 CAGAACGCCAACCCCGACTGCAAGACCATCCTGCGCGCTCTCGGCCCCGGCGCCCACCCTG 1020	901 CTGCGCGCCGAGCAGGCCAGCCCAGGACGTGAAGAACTGGATGACCGAGACCCTGCTGGTG 960	841 GACATCCGCCAGGGCCCCAAGGAGCCCTTCCGCGACTACGTGGACCGCCTTCTTCAAGACC 900	781 CGGTGGATCATCCTGGGCCTGAACAAGATCGTGCGGATGTACAGCCCCGTGAGCATCCTG 840	721 CAGGAGCAGATCGCCTGGATGACCAGCAACCCCCCGTGCCCGTGGGCGACATCTACAAG 780	661 GCCCCGGCCAGATGCGCGACCCCCGCGCGCAGCACCGACCACCAGCACCCTG 720	601 ACCATCAACGAGGAGGCCGCCGAGTGGGACCGCCTGCACCCCGTGCAGGCCCGGCCCCGTG 660	541 CTGAACACGATGTTGAACACCGTGGGCGGCCACCAGGCCGCCATGCAGATGCTGAAGGAC 600	481 TTCAGCCCCGAGGTGATCCCCCATGTTCACCGCCCTGAGCGAGGGCGCCCCCCCC	421 CACCAGGCCATCAGCCCCCGCACCCTGAACGCCTGGGTGAAGGTGATCGAGGAGAAGGCC 480	361 GCCGACGGCAAGGTGAGCCAGAACTACCCCATCGTGCAGAACCTGCAGGGCCAGATGGTG 420 	301 CTGGACAAGATCGAGGAGGAGCAGAACAAGTCCCAGCAGAAGACCCAGCAGGCCAAGGAG 360 	241 ACCGTGGCCACCCTGTACTGCGTGCACGCCGGCATCGAGGTCCGCGACACCAAGGAGGCC 300	181 ATGAAGCAGCTGCAGCCCGCCCTGCAGACCGGCACCGAGGAGCTGCGCAGCCTGTACAAC 240	121 CTGGAGGGCTTCGCCCTGAACCCCGGCCTGCTGGAGACCGCCGAGGGCTGCAAGCAA	

	gene	Bource	TITLE JOURNAL	JOURNAL REFERENCE AUTHORS	TITLE	REFERENCE AUTHORS	KEYWORDS SOURCE ORGANISM	DEFINITION ACCESSION VERSION	RESULT 7 AY181195	Qy 1 Db 1	Qу 1 рь 1	Qy 1 Db 1	Oy 1 Db 1	Qy 1 Db 1	0 1 Qy 1 1 Db 1
/codon_ftart=1 /transl_table=11 /transl_table=11 /product="gag_protein" /product="gag_protein" /protein_id="AAO65393.1" /db_xref="GI:37413993" /db_xref="GI:37413993" /translation="MGARASILRGGKLDKWEKIRLRPGGKKRYMIKHLVWASRELERF /translation="MGARASILRGGKLDKWEKIRLRPGGKKRYMIKHLVWASRELERF ALNPGLLETSEGCKQIMKQLQPALQTGTEELRSLYNTVATLYCVHEGVEVRDTKEALD RIESEQNKIQQKIQQAADGKVSQNYPIVQNLQGQMVHQKLSPRTLNAWVKVIEE KAPSPEVIPMFTALSEGATPQDLNTMLNTVGGHQAAMQMLKDTINEEAAEWDRLHPVH AGPIAPGQMREPRGSDIAGTTSTLQEQIAWMTSNPPIPVGDIYKRWIILGLNKIVRMY	usage	11485; /organism="synthetic construct" /mol_type="genomic DNA" /db_xref="taxon:32630"	Direct Submission  Submitted (16-NOV-2002) Medicine, Duke University Medical Center,  112 RPIII, LaSalle Street, Durham, NC 27710, USA  Location/Onalifiers	AIDS Res. Hum. Retroviruses 19 (9), 817-823 (2003)  2 (bases 1 to 1485)  Gao, F., Li, Y., Decker, J.M., Bibollet-Ruche, F., Rodenburg, C.M., Chen, Y., Shaw, D.R., Allen, S., Musonda, R., Shaw, G.M., Zajac, A.J. and	, Lecvin, N. and Hann, B.H. ion of HIV type 1 subtype xpression and immune resp	1485) Decker, J.M., Peyerl, F. Chen, Y., Shaw, D.R., A	synthetic construct synthetic construct	Synthetic construct HIV-1-derived gag protein (gag) gene, complete cds. AV181195 AV181195.1 GI:37413992	AVIAII95 1485 hn DNA linear SVN D	.498 CTGAGCCAGTAA 1509             .480 CTGAGCCAGTAA 1491	.438 GACCGCGAGCCCTACCGCGAGCCCCTGACCGCCCTGCGCAGCCTGTTCGGCAGCGGCCCC 1497	.378 CCCCCCGCCGAGAGCTTCCGCTTCGAGGAGACCACCCCCGCCCCAAGCAGGAGCCCAAG 1437	.321 CCCGGCAACTTCCTGCAGAACCGCAGCGAGCCCGCCGCCCCCACCGTGCCCACCGCC 1377	1261 GACTGCACCGAGCGCCAGGCCAACTTCCTGGGCAAGATCTGGCCCAGCCACAAGGGCCGC 1320	L141 GGCCCCCGCCGCGCGTGAAGTGCTTCAACTGCGGCCGCGAGGGGCCACATCGCCCGCAAC 1200 L201 TGCCGCGCCCCCCCGCAAGAAGGGGCTGCTGGAAGTGCGGCAAGGAGGGGCCACCAGATGAAG 1260
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α ω 4 ο O	715 ACCCTGCAGGAGCAGATCGCCTGGATGACCAGCAACCCCCCCGTGCCCGTGGGCGACATC	55 CCCGTGGCCCCGGCCAGATGCGCCGACCCCCCGCGGCAGCGACATCGCCGGCGCCCAGCCAG	595 AAGGACACCATCAACGAGGAGGCCGCCGAGTGGGACCGCCTGCACCCCGTGCAGGCCGGC	535 CAGGACCTGAACACGATGTTGAACACCGTGGGCGGCCACCAGGCCGCCATGCAGATGCTG	475 AAGGCCTTCAGCCCCGAGGTGATCCCCATGTTCACCGCCCTGAGCGAGGGCGCCACCCCCCCC	415 ATGGTGCACCAGGCCATCAGCCCCCGCACCCTGAACGCCTGGGTGAAGGTGATCGAGGAG	356 -AGGAGGCCGACGCCAAGGTGAGCCAGAACTACCCCATCGTGCAGAACCTGCAGGGCCAG	301 CTGGACAAGATCGAGGAGGAGGAGAACAAGTCCCAGCAGAAGACCCAGCAGCAGCAGCCA	241 ACCGTGGCCACCCTGTACTGCGTGCACGCCGGCATCGAGGTCCGCGACACCAAGGAGGCC	181 ATGAAGCAGCTGCAGCCCGCCCTGCAGACCGGCACCGAGGAGCTGCGCAGCCTGTACAAC	121 CTGGAGGGCTTCGCCCTGAACCCCGGCCTGCTGGAGACCGCCGAGGGGCTGCAAGCAGATC	61 CTGCGCCCCGGCGGCAAGAAGCACTACATGCTGAAGCACCTGGTGTGGGCCAGCCGCGAG	1 ATGGGCGCCCGCGCCAGCATCCTGCGCGGGGGAAAGCTGGACAAGTGGGAGAAGATCCGC	y Match 85.6%; Score 1291.4; DB 12; Length 1485; Local Similarity 92.6%; Pred. No. 2.7e-127; hes 1403; Conservative 0; Mismatches 76; Indels 36; Gaps	SPVSILDIKQGPKEPFRDYVDRFFKTLRAEQATQEVKNWMTDTLLVQNANPDCKTILK ALGPGATLEEMMTACQGVGGPSHKARVLAEAMSQTNSVNILMQKSNFKGNKRMVKCFN CGKEGHIARNCRAPRKKGCWKCGKEGHQMKDCTERQANFLGKIWPSHKGRPGNFLQNR PEPTAPPAESFRFEETTPAPKQESKDREALTSLKSLFGSDPLSQ"

Query Ma Best Loc Matches Matches Qy	FEATURES sourc	ORGANISM REFERENCE AUTHORS TITLE JOURNAL	AX455887 LOCUS DEFINITION ACCESSION VERSION KEYWORDS	Db Qy	A 4	Db Qy	Qy Vo	Qy db	Qy Db	Db Qy	g &	유 왕	D Qy
Match 84.6%; Score 1276.8; DB 6; Length 1479; ocal Similarity 92.5%; Pred. No. 9.2e-126; s 1399; Conservative 0; Mismatches 77; Indels 36; Gaps 4;  1 ATGGGCGCCGCGCCAGCATCCTGCGCGGGGAAAGCTGGACAAGTGGGAAAGATCCGC 60	e 11479 e 11479 /organism="synthetic cons/mol_type="unassigned DNA/db_xref="taxon:32630" /note="synthetic Gag of H	synthetic construct synthetic construct other sequences; artificial sequences.  1 zur Megede, J., Barnett, S.W., Engelbrecht, S. and van R Polynucleotides encoding antigenic hiv type c polypep polypeptides and uses thereof Patent: WO 0204493-A 3 17-JAN-2002;	AX455887 Sequence 3 from I AX455887 AX455887.1 GI:21	1495 CCCCTGAGCCAGTAA 1509 	1435 AAGGACCGCGAGCCCTACCGCGAGCCCCTGACCGCCAGCCTGCTTCGGCAGCGGC 1494	1375 GCCCCCCCCCGCCGAGAGCTTCCGCTTCGAGGAGACCACCCCCGCCCCAAGCAGGAGGCCC 1434	1315 GGCCGCCCGGCAACTTCCTGCAGAACCGCAGCGAGCCGAGCCGCCGCCGCCCACCGAGCCAACC 1374	1255 ATGAAGGACTGCACCGAGCGCCAGGCCAACTTCCTGGGCAAGATCTGGCCCAGCCACAAG 1314	1195 AAGAACTGCCGCGCCCCCCGCAAGAAGAGGGCTGCTGGAAGTGCGGCAAGGAGGGCCACCAG 1254	1135 TTCAAGGGCCCCCGGCGCAACGTCAAGTGCTTCAACTGCGGCAAGGAGGGCCACATCGCC 1194	1075 GTGCTGGCCGAGGCGATGAGCCCAAGGCGTGAACATCATGATGCAGAAGAGCAAC 1134	1015 ACCCTGGAGGAGATGATGACCGCCTGCCAGGGCGTGGGCGGCCCGGCCACAAGGCCCGC 1074	955 CTGGTGCAGAACGCCAACCCCGACTGCAAGACCATCCTGCGCGCTCTCGGCCCCGGCGCC 1014
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1018 CTGGAGGAGGATGACCGCCTGCCAGGGCGTGGCGCCACCAGGCCCACAAGGCCCCGCCTG 1077	B ACCCTGCGCCGAGCAGCCACCCAGGACGTGAAGAACTGGATGACCGAGACCCTGCTG	78 AAGCGGTGGATCATCCTGGGCCTGAACAAGATCGTGCGGATGTACAGCCCCGTGAGCATC	658 GTGGCCCCGGCCAGATGCGCGACCCCCGGGGGACACTCGCCGGCGCACCAGCACCACCAGCACCACCAGCAG	598 GACACCATCAACGAGGAGGCCGCCGAGTGGGACCGCCTGCACCCCGTGCAGGCCGGCC	538 GACCTGAACACGATGTTGAACACCGTGGGCGGCCACCAGGCCGCCATGCAGATGCTGAAG 597	478 GCCTTCAGCCCCGAGGTGATCCCCCATGTTCACCGCCCTGAGCGAGGGCGCCACCCCCCAG 537	418 GTGCACCAGGCCATCAGCCCCCGCACCCTGAACGCCTGGGTGAAGGTGATCGAGGAGAAG 477		301 CTGGACAAGATCGAGGAGGAGCAGAACAAGTCCCAGCAGAAGACCCAGCAGGAGGCCAAGGAG 360	241 ACCGTGGCCACCCTGTACTGCGTGCACGCCGGCATCGAGGTCCGCGACACCAAGGAGGCC 300	181 ATGAAGCAGCTGCAGCCCGCCCTGCAGACCGGCAGCCGAGGAGCTGCGCAGCCTGTACAAC 240	121 CTGGAGGGCTTCGCCCTGAACCCCGGCCTGCTGGAGACCGCCGAGGGCTGCAAGCAGATC 180	61 CTGCGCCCCGGCGCAAGAAGCACTACATGCTGAAGCACCTGGTGTGGGCCAGCCGCGAG 120                    61 CTGCGCCCCGGCGGCAAGAAGTGCTACATGATGAAGCACCTGGTGTGGGCCAGCCGCGAG 120

IBI ATCCGCCAGCTGCACCCCGCCCTGCAGACCGGCAGGAGCCTGAAGAGCCCTGTTCAAC 240	181 ATGAAGCAGCTGCAGCCCGCCCTGCAGACCGGCACCGAGGAGCTGCGCAGCCTGTACAAC 2	QY 121 CTGGAGGGCTTCGCCCTGAACCCCCGGCCTGCTGGAGACCGCCGAGGGCTGCAAGCAGATC 180	61 CTGCGCCCCGGCGAAGAAGTGCTACATGATGAAGCACCTGGTGTGGGCCAGCCGCGAG 12	61 .	ATGGGCCCCGCGCCAGCATCCTGCGCGGCGAGAAGCTGGAACAAGTGGGAGAAGATCCGC 6	Query Match 84.6%; Score 1276.8; DB 6; Length 1479; Best Local Similarity 92.5%; Pred. No. 9.2e-126; Matches 1399; Conservative 0; Mismatches 77; Indels 36; Gaps 4;	(	209-A 63 04-APR-2002; ION (US) on/Qualifiers	1 O'Hag Singh		TION Sequence 63 from Patent W00226209.  ION AX468543  N AX468543.1 GI:21901373	1470 h	Qy 1498 CTGAGCCAGTAA 1509               Db 1468 CTGAGCCAGTAA 1479	QY 1438 GACCGCGAGCCCTACCGCGAGCCCCTGACCGCCCTGCGCAGCCTGTTCGGCAGCGGCCCC 1497	QY 1378 CCCCCGCCGAGAGCTTCCGCTTCGAGGAGACCACCCCCGCCCCAAGCAGGAGCCCAAG 1437	Qy         1318         CGCCCCGGCAACTTCCTGCAGAACCGCAGCGAGCCGAGC	Qy 1258 AAGGACTGCACCGAGCGCCAGGCCAACTTCCTGGGCAAGATCTGGCCCAGGCCACAAGGGC 1317	QY 1198 AACTGCCGCGCCCCCCCCAAGAAGGGCCTGCTGGAAGTGCGGCAAGGAGGGCCACCAGATG 1257	Qy 1138 AAGGGCCCCCGGCGAACGTCAAGTGCTTCAACTGCGGCAAGGAGGGCCACATCGCCAAG 1197
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301 CTGGACAAGATCGAGGAGGAGCAGAACAAGTCCCAGCAGAAGACCCAGCAGGACAAGACCAAGGACAAGACCAAGGACCAAGGACCAAGGACAAGGACCAAGGACAAGGACCAAGGACAAGGACAAGGACAAGGACCAAGGAAGAA	4 4 0 0	Qy  61 CTGCGCCCCGGCGAAGAAGCACTACATGCTGAAGCACCTGGTGTGGGCCAGCCGCGAG 120	Query Match 84.2%; Score 1271.2; DB 6; Length 1479; Best Local Similarity 91.8%; Pred. No. 3.6e-125; Matches 1388; Conservative 10; Mismatches 78; Indels 36; Gaps 4;  Qy 1 ATGGGCCCGCCCAGCATCCTGCGCGAGAAGCTGGACAAGTGGGAGAAGATCCGC 60	e	ORGANISM Human immunodeficiency virus 1  ORGANISM Human immunodeficiency virus 1  Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate  lentivirus group.  REFERENCE 1  AUTHORS O'Hagan,D., Otten,G., Donnelly,J.J., Polo,J.M., Barnett,S.,  Singh,M., Ulmer,J. and Dubensky,T.W.  TITLE Microparticles for delivery of the heterologous nucleic acids  JOURNAL Patent: WO 0226209-A 67 04-APR-2002;	10 47 AX468547 1479 bp D TION Sequence 67 from Patent WO0226209. ION AX468547 QI:21901377	Qy       1498 CTGAGCCAGTAA 1509	QY 1438 GACCGCGAGCCCTACCGCGAGCCCCTGACCGCCCTGCGCAGCCTGTTCGGCAGCCGGCCCC 1497	QY 1378 CCCCCGCGAGAGCTTCCGCTTCGAGGAGACCACCCCCGCCCCAAGCAGGAGCCAAG 1437	
Q	B & B &	\$ 40 AG	\$ \$ \$ \$ \$	\$ \$ \$ \$ \$	S B & B &	D Q D Q	Db Qy	Db Qy	DB &9	Db
1378 CCCCCGCCGAGAGCTTCCGCTTCGAGGAGACCACCCCCCAAGCAGGAGCCCAAG 1437	1258 AAGGACTGCACCGAGCGCCAGGCCAACTTCCTGGGCAAGATCTGGCCCAGCCACAAGGGC 1317	9 9 8 8	CTGGAGGAGATGATGACCGCCTGCCAGGGCGTGGGCGGCCCCGGCCACAAGGCCCGCGTG	901 ACCCTGCGCGCGAGCAGAGCACCCAGGAGGTGAAGAACTGGATGACCGACACCCTGCTG 958 GTGCAGAACGCCAACCCCGACTGCAAGACCATCCTGCGCGCGC	у <u>н</u> —н р—р	GTGGCCCCGGCCAGATGCGCGACCCCCGCGCAGCACATCGCCGGCGCGCCACCACCACCACCACCACCACCACCACCA	598 GACACCATCAACGAGGAGGCCGCCGAGTGGGACCGCCTGCACCCCGTGCAGGCCGGCC	538 GACCTGAACACGATGTTGAACACCGTGGGCCGCCACCAGGCCGCCATGCAGATGCTGAAG 597	478 GCCTTCAGCCCCGAGGTGATCCCCATGTTCACCGCCCTGAGCGAGGGCGCCACCCCCCAG 537	

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  GACCTGAACACGATGTTGAACACCGTGGGCGGCCACCAGGCCGCCATGCAGATGCTGAAG
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/mol_type="unassigned DNA"
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Shao, Y.,
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The genome of the hiv-1 inter-subtype (c/b')
Patent: WO 0136614-A 2 25-MAY-2001;
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/mol_type="unassigned DNA"
/db_xref="taxon:12721"
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other sequences; artificial sequences.

1 (bases 1 to 1509)

RS zur Megede, J., Chen, M.C., Doe, B., Schaefer, M., Greselby, M., Otten, G.R. and Barnett, S.W.

Increased expression and immunogenicity of sequen immunodeficiency virus type 1 gag gene

J. Virol. 74 (6), 2628-2635 (2000)
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 zur Megede, J. and Barnett, S
Direct Submission
Submitted (04-NOV-1999) Vac
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/protein_id="AAF43628.1"
/protein_id="AAF43628.1"
/db_xref="GI:7248703"
/translation="mgarasvLsggelDkweKIRLRPGGKKKYKLKHIVWASRELERF
/translation="mgarasvLsggelDkweKIRLRPGGKKKYKLKHIVWASRELERF
AVNPGLLETSEGCRQILGQLQPSLQTGSEELRSLYNTVATLYCVHQRIDVKDTKEALE
KIEEEQNKSKKKAQQAAAAAGTGNSSQVSQNYPIVQNLQGQMVHQALSPRTLNAMVKV
VBEKAFSPEVIPMFSALSEGATPQDLNTMLNTVGGHQAAMQMLKETINEEAAEWDRVH
PVHAGPIAPGQMREPRGSDIAGTTSTLQEQIGWMTNNPPIPVGBIYKRWIILGLNKIV
RMYSPTSILDIRQGPKEPFRDYVDRFYKTLRAEQASQDVKNWMTETLLVQNANPDCKT
ILKALGPAATLEEMMTACQGVGGPGHKARVLAEAMSQVTNPATIMMQRGNFRNQRKTV
KCFNCGKEGHTARNCRAPRKKGCWRCGREGHQMKDCTERQANFLGKIWPSYKGRPGNF
LQSRPEPTAPPEESFRFGEEKTTPSQKQEPIDKELYPLTSLRSLFGNDPSSQ"
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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/transl_table:
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                                                                                                                  IS15 bp DNA linear PAT 17-JUL-2003 Improved expression of HIV polypeptides and production of virus-like particles.
other sequences; artificial sequences 1 (bases 1 to 1515)
Barnett,S., Megede,J.Z., Srivastava,I
                                              synthetic construct
synthetic construct
                                                                             BD263637.1 GI:33073405
JP 2002533124-A/4.
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    Srivastava, I.,
      Lian, Y.,
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Hartog, K.,

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Improved expression of HIV polypeptides and production of
virus-like particles

L Patent: JP 2002533124-A 4 08-OCT-2002;
CHIRON CORP
OS Artificial Sequence
PN JP 2002533124-A/4
PD 08-OCT-2002
PF 30-DEC-1999 JP 2000591193
PR 31-DEC-1999 US 60/114495,01-DEC-1999 US 60/168471 PI
SUSAN BARNETT,JAN ZUR MEGEDE,INDRESH SRIVASTAVA,YING LIAN, PI
KARIN HARTOG,
PI HONG LIU,CATHERINE GREER,MARK SELBY,CHRISTOPHER WALKER PC
C12N15/09,A61K31/711,A61K38/00,A61K48/00,A61P31/18,A61P37/02, PC
C12N5/10,
PC C12N7/00,C12P21/02,C12N15/00,C12N5/00,A61K37/02 CC
Description of Artificial Sequence: synthetic HIV-Gag FH Key
Location/Qualifiers
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Similarity 88.5%;
51; Conservative
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                                               GCCACCCCAGGACCTGAACACGATGTTGAACACCGTGGGCGGCCACCAGGCCGCCATG
                                                                 GCCACCCCCAGGACCTGAACACGATGTTGAACACCGTGGGCGGCCACCAGGCCGCCATG
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Improved expression of HIV polypeptides and production of virus-like particles
Patent: EP 1433651-A 4 30-JUN-2004;
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Similarity 88.5%;
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/mol_type="unassigned DNA"
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/note="Description of Artificial Sequence: synthetic HIV-Gag"
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Search completed: March 12, 2005, 21:18:23 Job time : 6741.44 secs

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3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

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GENERAL ANTONIES.

APPLICANT: BARNETT, Susan

APPLICANT: ZUR MEGEDE, Jan

APPLICANT: SRIVASTAVA, Indresh

APPLICANT: LIAN, Ying

APPLICANT: HARTOG, Karin

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APPLICANT: LIU, Hong

APPLICANT: SELBY, Mark

APPLICANT: SELBY, Mark

APPLICANT: WALKER, Christopher

TITLE OF INVENTION: OF VIRUS-LIKE PARTICLES

FILTE FILTERENCE: 1621.002

CURRENT APPLICATION NUMBER: US/09/475,515A

CURRENT FILING DATE: 1999-12-30

NUMBER OF SEQ ID NOS: 90

SOFTWARE: Patentin Ver. 2.0

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OTHER INFORMATION: Description of Artificial Sequence:

OTHER INFORMATION: gp160.modUS4.delV1/V2.gag.modSF2
US-09-475-515-75
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GENERAL INFORMATION:
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TYPE: DNA
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                                                                                                                                                                   GGCCACATCGCCCAAGAACTGCCGCGCCCCCCCCCAAGAAGGGGCTGCTGGAAGTGCGGCAAG
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GENERAL INFORMATION:
APPLICANT: BARNETT, SUBAN
APPLICANT: ZUR MEGEDE, Jan
APPLICANT: SRIVASTAVA, Indresh
APPLICANT: LIAN, Ying
APPLICANT: LIAN, Ying
APPLICANT: HARTOG, Karin
APPLICANT: HARTOG, Karin
APPLICANT: SELBY, Mark
APPLICANT: SELBY, Mark
APPLICANT: WALKER, Christopher
TITLE OF INVENTION: IMPROVED EXPRESSION OF HIV POLYPEPTIDES AND PRODUCTION
TITLE OF INVENTION: OF VIRUS-LIKE PARTICLES
FILE REFERENCE: 1621.002
CURRENT APPLICATION NUMBER: US/09/475,515A
CURRENT FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 90
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 76
LENGTH: 4608
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OTHER INFORMATION: gp160.modSF162.delV2.gag.modSF2
US-09-475-515-76
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Best Local Similarity
Matches 1351; Conserv
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APPLICANT: LIAN, Ying
APPLICANT: HARTOG, Karin
APPLICANT: SELBY, Mark
APPLICANT: SELBY, Mark
APPLICANT: WALKER, Christopher
ITILE OF INVENTION: IMPROVED EXPRESSION OF HIV POLYPEPTIDES AND PRODUCTION
ITILE OF INVENTION OF VIRUS-LIKE PARTICLES
FILE REFERENCE: 1621.002
CURRENT APPLICATION NUMBER: US/09/475,515A
CURRENT FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 90
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GCCACCCCCAGGACCTGAACACGATGTTGAACACCGTGGGCGGCCACCAGGCCGCCATG 585
                               GTGGAGGAGAAGGCCTTCAGCCCCGAGGTGATCCCCATGTTCAGCGCCCTGAGCGAGGGC
                                                            ATCGAGGAGAAGGCCTTCAGCCCCGAGGTGATCCCCCATGTTCACCGCCCTGAGCGAGGGC
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nilarity 88.5%;
Conservative
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Pred. No. 2.8e-173;
0; Mismatches 140;
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RESULT 5
US-09-475-515-73
; Sequence 73, Application
; Patent No. 6602705
; GENERAL INFORMATION:
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APPLICANT: BARNETT, SUBAN
APPLICANT: ZUR MEGEDE, Jan
APPLICANT: SRIVASTAVA, Indresh
APPLICANT: LIAN, Ying
APPLICANT: HARTOG, Karin
APPLICANT: HARTOG, Karin
APPLICANT: SELBY, Hong
APPLICANT: SELBY, Mark
APPLICANT: SELBY, Mark
APPLICANT: WALKER, Christopher
TITLE OF INVENTION: OF VIRUS-LIKE PARTICLES
FILE REFERENCE: 1621.002
CURRENT APPLICATION NUMBER: US/09/475,515A
CURRENT FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 90
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 73
LENGTH: 4766
TWORD- NAM ; OTHER INFORMATION: Description of Artificial Sequence: ; OTHER INFORMATION: gp160.modUS4.gag.modSF2 US-09-475-515-73 GCCGACGGCA-------AGGTGAGCCAGAACTACCCCATCGTGCAGAACCTG CAGATGCTGAAGGAGACCATCAACGAGGAGGCCGCCGAGTGGGACCGCGTGCACCCCGTG CAGATGCTGAAGGACACCATCAACGAGGAGGCCGCCGAGTGGGACCGCCTGCACCCCGTG ATGAAGCAGCTGCAGCCCGCCCTGCAGACCCGGCACCGAGGAGCTGCGCAGCCTGTACAAC ATGGGCGCCCGCGCAGCATCCTGCGCGCGAGAAAGCTGGACAAGTGGGAGAAGATCCGC GCCACCCCCAGGACCTGAACACGATGTTGAACACCGTGGGCGGCCACCAGGCCGCCATG GCCACCCCCAGGACCTGAACACGATGTTGAACACCGTGGGCGGCCACCAGGCCGCCATG GTGGAGGAGAAGGCCTTCAGCCCCGAGGTGATCCCCATGTTCAGCGCCCTGAGCGAGGGC ATCGAGGAGAAGGCCTTCAGCCCCGAGGTGATCCCCCATGTTCACCGCCCTGAGCGAGGGGC CTGGAGAAGATCGAGGAGGAGCAGAACAAGTCCAAGAAGAAGGCCCAGCAGCAGCCGCCCCCCC CTGGACAAGATCGAGGAGGAGCAGAACAAGTCCCAGCAGAAGAACCCCAGCAGGAGGAG ACCGTGGCCACCCTGTACTGCGTGCACGCCGGCATCGAGGTCCGCGACACACCAAGGAGGCC CTGGGCCAGCCGAGCCTGCAGACCGGCAGCGAGGAGCTGCGCAGCCTGTACAAC CTGGAGCGCTTCGCCGTGAACCCCGGCCTGCTGGAGACCAGCGAGGGCTGCCGCCAGATC CTGGAGGGCTTCGCCCTGAACCCCGGCCTGCTGGAGACCGCCGAGGGGCTGCAAGCAGATC CTGCGCCCCGGCCAAGAAGAAGTACAAGCTGAAGCACATCGTGTGGGCCAGCCGCGAG CTGCGCCCCGGCGGCAAGAAGCACTACATGCTGAAGCACCTGGTGTGGGCCCAGCCGCGAG ATGGGCGCCCGCGCCAGCGTGCTGAGCGGCGGCGAGCTGGACAAGTGGGAGAAGATCCGC **ACCGTGGCCACCCTGTACTGCGTGCACCAGCGCATCGACGTCAAGGACACCAAGGAGGACCC** 79.6%; nilarity 88.5%; Conservative Sequence Score 1201; DB 4; Pred. No. 2.8e-173; 0; Mismatches 140; Length 4766; Indels 36; 645 3892 3832 585 465 405 360 300 3772 525 3712 3652 3592 3532 3472 240 3412 180 3352 120 3292

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RESULT 6
US-09-475-515-7
; Sequence 7, Application US/094755; Patent No. 6602705; GENERAL INFORMATION:
; APPLICANT: BARNETT, SUSAN; APPLICANT: ZUR MEGEDE, Jan; APPLICANT: SRIVASTAVA, Indresh; APPLICANT: LIAN, Ying; APPLICANT: HARTOG, Karin; APPLICANT: LIU, Hong; APPLICANT: LIU, GREER, Catherine
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; OTHER INFORMATION: Description of Artificial Sequence: ; OTHER INFORMATION: HIV-Gag/HCV-core fusion polypeptide US-09-475-515-7
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APPLICANT: WALKER, Christopher
TITLE OF INVENTION: IMPROVED EXPRESSION OF HIV POLYPEPTIDES AND PRODUCTION
TITLE OF INVENTION: OF VIRUS-LIKE PARTICLES
FILE REFERENCE: 1621.002
CURRENT APPLICATION NUMBER: US/09/475,515A
CURRENT FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 90
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
LENGTH: 2031
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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Pred. No. 5.6e-173;
D; Mismatches 140;
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RESULT 7

US-09-475-515-5

US-09-475-515-5

; Sequence 5, Application US/09475515A

; Patent No. 6602705

; GENERAL INFORMATION:

APPLICANT: BARNETT, Susan

APPLICANT: ZUR MEGEDE, Jan

APPLICANT: LIAN, Ying

APPLICANT: LIAN, Ying

APPLICANT: LIU, Hong

APPLICANT: SELBY, Mark

APPLICANT: SELBY, Mark

APPLICANT: WALKER, Christopher

TITLE OF INVENTION: OF VIRUS-LIKE PARTICLES

FILE REFERENCE: 1621.002

CURRENT APPLICATION NUMBER: US/09/475,515A

CURRENT FILING DATE: 1999-12-30
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; OTHER INFORMATION: Description of Artificial Sequence: synthetic; OTHER INFORMATION: HIV-Gag-protease US-09-475-515-5
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; SOFTWARE: PatentIn Ver.
; SEQ ID NO 5
; LENGTH: 1853
; TYPE: DNA
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; FEATURE:
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Pred. No. 1e-160;
0; Mismatches 192;
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Sequence 78, Application US/09475515A; Patent No. 6602705; GENERAL INFORMATION:
APPLICANT: BARNETT, Susan; APPLICANT: SIVASTAVA, Indresh; APPLICANT: LIAN, Ying; APPLICANT: LIU, Hong; APPLICANT: BELBY, Mark
APPLICANT: SELBY, Mark
APPLICANT: WALKER, Christopher
TITLE OF INVENTION: IMPROVED EXPRESSION OF HIV POI; TITLE OF INVENTION: OF VIRUS-LIKE PARTICLES; FILE REFERENCE: 1621.002; CURRENT APPLICATION NUMBER: US/09/475,515A; CURRENT FILING DATE: 1999-12-30; NUMBER OF SEQ ID NOS: 90
SOFTWARE: Patentin Ver. 2.0
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; OTHER INFORMATION: Description of Artificial Sequence: US-09-475-515-78
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Query Match 74.1%; Score 1117.8; DB 4; Length 1865; Best Local Similarity 85.1%; Pred. No. 1e-160; Matches 1299; Conservative 0; Mismatches 192; Indels 36; Gaps 3; Qy 1 ATGGGCGCCCGCGCCAGCATCCTGCGCGCGAGAAGCTGGACAAGTGGGAGAAGATCCGC 60	; TYPE: DNA ; ORGANISM: Artificial Sequence ; ORGANISM: Artificial Sequence ; FEATURE: ; FEATURE: ; OTHER INFORMATION: Description of Artificial Sequence: GP2 US-09-475-515-79	SOFTWARE: PatentIn Ver. 2.0  SEQ ID NO 79  LENGTH: 1865	FILE REFERENCE: 1621.002 CURRENT APPLICATION NUMBER: US/09/475,515A CURRENT FILING DATE: 1999-12-30	APPLICANT: SELBY, Mark APPLICANT: WALKER, Christopher TITLE OF INVENTION: IMPROVED EXPRESSION OF HIV POLYPEPTIDES AND PRODUCTION TITLE OF INVENTION: OF VIRUS-LIKE PARTICLES	APPLICANT: LIAN, Ying APPLICANT: HARTOG, Karin APPLICANT: LIU, Hong APPLICANT: GREER, Catherine		RESULT 9 US-09-475-515-79 ; Sequence 79, Application US/09475515A ; Patent No. 6602705	Db 1495 TTTGGCAACGACCCCTCGTCACAGTAA 1521	1435 TCTCAGAAGCAGGAGCCGATAGACAAGG			1273 GAAGGACACCAAATGAAAGATTGCACTGAGAGACAGGCTAATTTTTTTAGGGAAGATCTGG	183 GECCACATCACCANGRACISCESCECCCCCCCARGARGGGCIGCIGGARGIGCGGCAAG 124 213 GGCCACACCGCCAGGAACTGCCGCGCCCCCCGCAAGAAGGGCTGCTGGCGCCAAGACATCTGCCGCCGC 127	1123 CARAMENTE I CHANGESC COCCARCIS CARACISC I CARCISC GENERAL I I I I I I I I I I I I I I I I I I I	1133 CACAGGEGACCTGCCCGGGGAGGCGACCAGGTGACCCGGGGACCATCATGATG 115	بر د	Db 973 GAGACCCTGCTGGTGCAGAACGCCAACCCCGACTGCAAGACCATCCTGAAGGCTCTCGGC 1032  OY 1006 CCCGGCGCCACCCTGGAGGAGATGATGACCGCCTGCCAGGGCGTGGGCGGCCCCGGCCAC 1065
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APPLICANT: BARNETT, Susan
APPLICANT: SRIVASTAVA, Indresh
APPLICANT: SRIVASTAVA, Indresh
APPLICANT: LIN, Ying
APPLICANT: LIN, Ying
APPLICANT: LIU, Hong
APPLICANT: HARTOG, Karin
APPLICANT: GREER, Catherine
APPLICANT: SELEY, Mark
APPLICANT: WALKER, Christopher
TITLE OF INVENTION: IMPROVED EXPRESSION OF HIV POLYPEPTIDES AND PRODUCTION
TITLE OF INVENTION: MYMBER: US/09/475,515A
CURRENT FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOMBER: US/09/475,515A
CURRENT FILING DATE: 1999-12-30
SOFTWARE: PATENTIN Ver. 2.0
SOFTWARE: PATENTIN Ver. 2.0
SOFTWARE: A319
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
OTHER INFORMATION: HIV-Gag-polymerase
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Matches 1299; Conserv
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  GGCCACATCGCCAAGAACTGCCGCGCCCCCCGCAAGAAGGGGCTGCTGGAAGTGCGGCAAG
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                                                   CAGCGCGGCÁACTTCCGCAACCAGCGGAAGÁCCGTCAÁGTGCTTCAACTGCGGCAAGGAG
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1146; Conservative 0; Mismatches 98  1 ATGGCGCCCGCGCCCAGCATCCTGCGGCGCGAGAAGCT	H: 1268  DNA  DNA  ISM: Artificial Sequence  RE:  INFORMATION: Description of Artificial Sequence: synthetic Gag  INFORMATION: common region  -515-9  atch  69.5%; Score 1049.2; DB 4; Length 1268;  cal Similarity 90.8%; Pred. No. 2.4e-150;	APPLICANT: APPLICANT: TITLE OF I TITLE OF I FILE REFER CURRENT AP CURRENT FI NUMBER OF SOFTWARE:	O. 6602705 INFORMATION: NT: BARNETT, SUB NT: ZUR MEGEDE, NT: SRIVASTAVA, NT: LIAN, Ying NT: HARTOG, Kari NT: LIU, Hong NT: GREER, Cathe	Qy 1483 TTCGGCAGCGCCCCTGAGCCAGTAA 1509	1363 ACCGTGCCCACCGCCCCCCCCGCGAGA	1303 CCCAGCCACAAGGGCCGCCCCGGCAACTTCCTGCAGAACCGCAGCGAGCCCGCCC	
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US-09-952-060-27
Sequence 27, Application US/09952060
Patent No. 6733993
GENERAL INFORMATION:
APPLICANT: Emini, Emilio A.
APPLICANT: Emini, Rima
APPLICANT: Youli, Rima
APPLICANT: Youli, Rima
APPLICANT: Shiver, John W.
APPLICANT: Kaslow, David C.
APPLICANT: Kaslow, David C.
APPLICANT: Cohen, Ling
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APPLICANT: Cohen, Tinothy J.
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APPLICANT: Wallow, David C.
APPLICANT: Cohen, Ling
APPLICANT: Wallow, David C.
APPLICANT: Cohen, Ling
TITLE OF INVENTION: WACCINES EXPRESSING CODON OPTIMIZED HIVI
TITLE OF INVENTION: WODIFICATIONS
FILE REFERENCE: 20747Y
CURRENT APPLICATION NUMBER: US/09/952,060
CURRENT APPLICATION NUMBER: PCT/US01/28861
PRIOR APPLICATION NUMBER: FCT/US01/28861
PRIOR APPLICATION NUMBER: 60/317,814
PRIOR APPLICATION NUMBER: 60/317,816
PRIOR FILING DATE: 2001-09-15
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PastESEQ for Windows Version 4.0
SEQ ID NO 27
LENGTH: 1521
TYDE: DNA
CORANISM: Artificial Sequence
FEATURE:
COTHER INFORMATION: Codon optimized DNA encoding human HIV-1
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Matches 1210; Conservative
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«ESULT 13
US-09-974-702-1
; Sequence 1, Application US,...
; Patent No. 6696291
; GENERAL INFORMATION:
    APPLICANT: Shiver, John W.
    Davies, Mary Ellen
    Freed, Daniel C.
    '''', Margaret A.
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Best Local Simi
Matches 1210;
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FASELSEQ for Windows Version 2.0
CURRENT APPLICATION NUMBER: US/09/974,702
FILING DATE: 09-Oct-2001
CLASSIFICATION DATA:
APPLICATION NUMBER: 09/017,981
FILING DATE: 03-FEB-1998
APPLICATION NUMBER: US60/037,854
FILING DATE: 07-FEB-1997
APPLICATION NUMBER: GB9705040.5
FILING DATE: 12-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hand, J. Mark
REGISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 19730
TELEPHONE: 732-594-3905
TELEPHONE: 732-594-4720
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TITLE OF INVENTION: Synthetic HIV Ga
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000, 126 E. L
CITY: Rahway
                                                                                                                                                                                                                                                                                                                                 LENGTH: 1532 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: both
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
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                                   COUNTRY: USA
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Pred. No. 1.4e-138;
0; Mismatches 281;
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Sequence 25, Application US/09952060

Sequence 25, Application US/09952060

Sequence 25, Application US/09952060

Sequence 25, Application US/09952060

Sequence 25, Applicant No. 6733993

GENERAL INFORMATION:

APPLICANT: Coull, Rima
APPLICANT: Chen, Ling
APPLICANT: Shiver, John W.
APPLICANT: Shiver, John W.
APPLICANT: Casimiro, David C.
APPLICANT: Casimiro, David C.
APPLICANT: Casimiro, David C.
APPLICANT: Cosimiro, David C.
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APPLICANT: Shiver, John W.
APPLICANT: Cosimiro, David C.
APPLICANT: WACCINES EXPRESSING CODON OPTIMIZED HIV1-GAG, POL,
TITLE OF INVENTION: WACCINES EXPRESSING CODON OPTIMIZED HIV1-GAG, POL,
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PRIOR FILING DATE: 2001-09-14
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PRIOR FILING DATE: 2001-03-27
PRIOR APPLICATION NUMBER: 60/217,056
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ALIGNMENTS

## JOURNAL REFERENCE AUTHORS TITLE REFERENCE AUTHORS TITLE ACCESSION VERSION KEYWORDS SOURCE ORGANISM RESULT 1 AG332984/c LOCUS DEFINITION FEATURES COMMENT JOURNAL source Vector R.Site R.Site and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (B-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170) Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp). Tsukuba Institude, Bio Resource Center, The Institute of physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan phone: 81-298-36-9199 2 (bases 1 to 1440) Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y. Direct Submission Mus musculus molossinus Mus musculus molossinus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus Sequencing : T7 LIBRARY Mus musculus Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical Hattori, M., PRIMERS e-mail: abe@rtc.riken.jp Unpublished BAC end Sequences AG332984.1 Location/Qualifiers /organism="Mus musculus molossinus" /mol\_type="genomic DNA" /sub\_species="molossinus" /db\_xref="taxon:57486" tissue\_type="mixture of kidney and spleen" /clone\_lib="MSMg01 Mouse Male BAC Library" /clone="MSMg01-123F20.T7" /sex="male" : pBACe3.6 : ECORI : ECORI. Toyoda,A., Noguchi,H., Kojima,T. uences of Library MSMg01 GI:47906294 molossinus 1440 DNA, bp DNA linear G clone:MSMg01-123F20.T7, Sakaki,Y. GSS 02-JUN-2004 7, genomic survey

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Best Local Similarity 44.4%;
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Department of Bioinformatic
Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 10
Tel: 86-10-80481559
Fax: 86-10-80488676
Email: chenchen@genomics.org.cn
Rice genomic sequence.
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Oryza sativa (indica cultivar-group)
Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 1941)
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/mol_type="genomic DNA"
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Resnick, A., Fraser, C.M., Yuan, Y., S
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/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="zmmBTa458K20"
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Contact: Cordonnier-Fratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
Tel: 706 542 1860
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826 bp mRNA linear EST 01-API RHOH1_32_C05.g1_A002 Acid- and alkaline-treated roots Sorghum bicolor cDNA clone RHOH1_32_C05_A002 5', mRNA sequence.
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1 (bases 1 to 826)
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CN128942.1 GI:45956257
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              TGCGCCCCGGCGAAGAAGCACTACATGCTGAAGCACCTGGTGTGGGCCAGCCGCGAGC
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Location/Qualifiers
                                                                                                                                                                                                                               5.4%;
ilarity 47.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="RHOH1 32 C05 A002"
/clone="RHOH1 32 C05 A002"
/clone lib="Acid- and alkaline-treated roots"
/clone lib="Acid- and alkaline-treated roots"
/note="Organ: Root; Vector: pME18S-FL3; Site 1: XhoI;
Site 2: XhoI; The library was prepared from polyA+ RNA
from 8-day-old roots harvested from BTx623 sorghum
seedlings grown in hydroponic culture. HCl was added to a
pH of 3.0 to some seedlings, KOH to a pH of 9.0 for
others. Roots were harvested 3, 12 and 27 hr after
addition and pooled for RNA preparation. Double-stranded
cDNA was cloned unidirectionally into different DraIII
sites of the pME18S-FL3 vector (5-prime DraIII site is
CACTGTGTG, 3-prime DraIII site is CACCATGTGG). XhoI excises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/cultivar="BTx623"
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                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA insert."
                                                                                                                                                                                                                                     <u>,</u>
                                                                                                                                                                                                                            Score 81.6; DB 7;
Pred. No. 9.9e-05;
0; Mismatches 394;
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                                                                                                                                                                                                                                                                                                                                                                                              Gasterosteus aculeatus (three spined stickleback)
Gasterosteus aculeatus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes;
Gasterosteidae; Gasterosteus.
Beckman Center B300, 279
Tel: 650 725 5954
Fax: 650 725 7739
                                                                                                                                                                                Kingsley,D.M., Peichel,C.,
Schmutz,J. and Myers,R.M.
Expressed sequence tags fro
Unpublished (2003)
Contact: Kingsley, DM
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                                                                                                               HHMI and Department of Developmental Biology Stanford University School of Medicine
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High quality sequence start: 4
High quality sequence stop: 792.
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CCGGCGCAACGTCAAGTGCTTCAACTGCGGCAAGGAGGGCCACATCGCCAAGAACTGCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="heads and internal organs combined"
/dev_stage="adult"
/clone_lib="SHGC-CDA"
/note="Vector: lambda ZAP Express/pBK-CMV; Site_1: EcoR1
(5' adaptor); Site_2: XhoI (3' linker primer); The mixed
organ cDNA library was generated using the ZAP-cDNA method
by Stratagene. First strand cDNA synthesis was primed with
a a 50 bp linker primer containing an oligo dT sequence
preceded by a synthetic XhoI site. 5 prime adaptors were
used containing an EcoR1 cohesive end. The finished cDNAs
were inserted in to the ZAP express vector
unidirectionally in the sense orientation with respect to
the lac2 promoter of pBK-CMV. An amplified library was
prepared from approximately 3 million primary clones in
the lambda ZAP Express vector. In vivo excision was then
used to generate individual pBK-CMV phagemid clones for
EST sequencing."
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/db_xref="taxon:69293"
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|mol_type="mRNA"
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Jiao,Y., Sun,N., Zhang,X., Bao,J., Sun,D.,
Wong,G.K.S., Deng,X.W. and Wang,J.
An analysis of transcriptional regulation of
its comparison to Arabidopsis
Unpublished (2004)
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Oryza sativa (indica cultivar-group)
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Department of Bioinformatic
Beijing Institute of Genomics
Chinese Academy of Sciences, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 1800)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 86-10-80481559
Fax: 86-10-80488676
                                                                                                                                                                                                                                                                                                                                                                                                                                  Rice genomic sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: chenchen@genomics.org
                                GGGCTGCAAGCAGATCATGAAGCAGCTGCAGCCCGCCCTGCAGACCGGCACCGAGGAGCT 224
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                                                                   GTGGGCCAGCCGCGAGCTGGAGGGCTTCGCCCTGAACCCCGGCCTGCTGGAGACCGCCGA 164
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/mol_type="genomic DNA"
/db_xref="taxon:39946"
/clone_lib="Oryza sativa Express
/note="Oryza sativa exon trapped
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     CL974989 2031 bp DNA linear GSS 21-SEP-OSIFCC042895 Oryza sativa Express Library Oryza sativa (indica cultivar-group) genomic, genomic survey sequence.
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Ma,L., Wangc,J., Chen,C., Liu,X., Su,N., Li,L., Wang,X., Cao, Jiao,Y., Sun,N., Zhang,X., Bao,J., Sun,D., Zhao,H., Yuan,L., Wong,G.K.S., Deng,X.W. and Wang,J.
An analysis of transcriptional regulation of the rice genome its comparison to Arabidopsis
Unpublished (2004)
Contact: Chen Chen
Department of Bioinformatic
Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: chenchen@genomics.org.
Rice genomic sequence.
Class: exon-trapped.
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Fax: 86-10-80488676
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/mol_type="genomic DNA"
/db_xref="taxon:39946"
/clone_lib="Oryza sativa E
/note="Oryza sativa exon t
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**sequences** 

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372

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AUTHORS
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                                                                                        Email: oandersn@pw.usda.gov
Sequences have been trimmed
quality sequence with phred
Seq primer: SK primer
                                                                                                                                                                                                                                                  Pooideae; Triticeae; Triticum.

1 (bases 1 to 749)

1 (bases 1 to 749)

Anderson,O.D., Akhunov,E., Chao,S., Crossman,C., Deal,K.,

Dvorak,J., Lazo,G.R., Pham,J., Rausch,C.J., Wilson,C. and Woo,J.

The structure and function of the expressed portion of the wheat
genomes - Salt-stressed root cDNA library
Unpublished (2002)
                                                                                                                                                                                Contact: Olin Anderson
US Department of Agriculture, Agriculture Research
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
                                                                                                                                                                                                                                                                                                                                                                                                                        BQ744212

BQ744212

WHE4113_A01_A01ZS Wheat salt-stressed root cDNA library Triticum aestivum cDNA clone WHE4113_A01_A01, mRNA sequence.

BQ744212

BQ744212.1 GI:21890999

EST.
                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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                                                                                                              score less than 20
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/clone_lib="Wheat salt-stressed root cDNA library"
/clone_lib="Wheat salt-stressed root cDNA library"
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pBluescript SK(-); Site_1: ECORI; Site_2: XhoI; Hydroponic
pBluescript SK(-); Site_1: CORIF SITE_2: XhoI; Hydroponic
pBluescript of California, Davis (E. Akhunov
and NaCl for either 12 hours or 7 days. Root tissues of the
plants gubjected to both types of treatment were collected
separately at University of California, a cDNA library was prepared
separately from the two samples (12h and 7day treatments),
and equal amount of RNA was then pooled. PolyA RNA was
purified from the pooled RNA, a cDNA library was made, and
the cDNA clones were in vivo excised to give pBluescript
SK(-) phagemids in J. Dvorak's lab (E. Akhunov, J. Dvorak)
at the University of California, Davis. Colony plating,
plasmid DNA preparations and DNA sequencing were performed
in the OD Anderson lab (all other authors)."
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CCAAG GEGRACCECTECACCCCGTGCAGGCCGGCCCGTGGCCCCGGCCAGATGCGCGACCCCC GCGGCCACCAGGCCGCCATGCAGATGCTGAAGGACACCATCAACGAGGAGGCCGCCGAGT GCGAGGCCGAGAAGGAGCGCCCCCCCGCGCGAGCGCCACTACCAGAACCACCGCTCCCACC CCATCGTGCAGAACCTGCAGGGCCAGATGGTGCACCAGGCCATCAGCCCCCGCACCCTGA 448 GCTTCAACCAGCGCCCCAGCTCCCCCAGCGCGCGACGAGGAGGTCGAGGCCAAGCGCC AGTCCCAGCAGAAGACCCCAGCAGGCCAAGGAGGCCGACGGCAAGGTGAGCCAGAACTACC CCTTCAGCCTCGTCGACGCCAAGCCGCCCAAGCACCCGCGCTTCGGGCCCAAGTGGC CCGGCATCGAGGTCCGCGACACCAAGGAGGCCCTGGACAAGATCGAGGAGGAGCAGAACA 328 CCTGGGACATTGTCGTGCAGCGCGTCGGCAACAAGCTCTTCTTCGACAAGCGCGAGGGCT GCCTGAACAAGATCGTGCGGATGTACAGCCCCGTGAGCATCCTGGACATCCGCCAGGGCC CCGTCTTCGCCACCGACGCCATCCTCGCCGCCCTCATGTGCACGCCCCGCAGCATCCTCT GGATGACCAGCAACCCCCCCGTGCCCGTGGGCGACATCTACAAGCGGTGGATCATCCTGG TCAAGATCACCACCACCACGACGACCCCATCATCCGCCGCCTCGCCGAGGAGGACAAGGCCA GCGGCAGCGACATCGCCGGCGCCCACCAGCACCCTGC-----AGGAGCAGATCGCCT ACGACCGCGTCAACCCCCAAGACGGCCCGCCGCCTCGAGCGCCTTCAAGAACCGCCAGTTCT TCGCCGACCAGCCCGAGGACCTGCTCGTCTGCGGCGCCGTCGACTCGTACGACCGCGCCT CCGACTGGACCATCCTCGAGCAGATCCCCTTCGCCAACTTCACCAAGCTCTCCCTTCGCCG TCACCGCCCTGAGCGAGGGCGCCACCCCCCAGGACCTGAACACGATGTTGAACACCGTGG ACCACCAGGGCTTCCGCGGCAACCAGCAGAACACCGCCAAGCCCTCCGTCGACATCCAGC ACGCCTGGG---TGAAGGTGATCGAGGAGAAGGCCCTTCAGCCCCGAGGTGATCCCCATGT Conservative 861 612 5.48; <u>.</u> Score 81; DB 5; Length 749; Pred. No. 0.00013; 0; Mismatches 300; Indels 12; Gaps 856 547 487 625 607 427 685 367 565 505 187 127 388 736 307 247 67

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BE636712

ON rockefeller.0.42 Mastigamoeba balamuthi lambda ZAP II Library
Mastigamoeba balamuthi cDNA similar to vacuolar ATP synthase
subunit B (EC 3.6.1.3), mRNA sequence.

BE636712

BE636712.1 GI:9919823

EST.

Mastigamoeba balamuthi
SM Mastigamoeba balamuthi
Eukaryota; Pelobiontida; Mastigamoebidae; Mastigamoeba
E 1 (bases 1 to 1674)

E 1 (bases 1 to 1674)

B Bapteste, E., Brinkmann, H., Lee, J.A., Moore, D.V., Sensen, C.W.,
Philinne H

Durufle, L., Gaasterland, T., Lopez, P., Muller, M. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Laboratory of Biochemical Parasitology
The Rockefeller University
1230 York Avenue, New York, NY 10021, [
Email: mmuller@rockvax.rockefeller.edu
Insert Length: 1674 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The analysis of 100 genes supports the grouping of three highly divergent amoebae: Dictyostelium, Entamoeba, and Mastigamoeba Proc. Natl. Acad. Sci. U.S.A. 99 (3), 1414-1419 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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Laboratory of Biochemical Parasitology
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                                                                                                  GCGCCATCGACACGATGAACTCGATCGCCCGTGGCCAGAAGATCCCGCTGTTCAGCGCCG
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Pred. No. 0.00015;
0; Mismatches 756;
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1 (bases 1 to 746)

2 (cosby, W.L., Danyluk, J., Eudes, F., Frick, M., Gaudet, D., Genswein, B., Graf, R., Gulick, P., Hrycan, L.D., Laroche, A., Links, M.G., McCarthy, E.L., Monroy, A., Muzak, I., Nilson, D., Penniket, C., Rocach, J.L. and Sarhan, F.

Functional Genomics of Abiotic Stress In Wheat and Canola Crops Impublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (default parameters) has been run on this sequence. Lucy identified the region [13,662]. Plate: L6B016 row: K column: 15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  University of Saskatchewan, Department of Computer Science 1C101 Engineering Building, 57 Campus Drive, Saskatoon, Saskatchewan, S7N SA9, Canada Tel: 306 966 1769
Fax: 306 966 2033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: fgas_ests@cs.usask.ca
This sequence is the direct result of the phred (default parameters). It is the raw identification of the high quality insert
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                                                                     CCCTGTACTGCGTGCACGCCGGCATCGAGGTCCGCGACACCAAGGAGGCCCTGGACAAGA 310
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If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of t maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB:
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/note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"
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Fax: 306 966 2033
Email: fgas_ests@cs.usask.ca
This sequence is the direct result of the Base calling software Phred (default parameters). It is the raw base calls. To aid in the identification of the high quality insert the software Lucy (default parameters) has been run on this sequence. Lucy identified the region [12,750].
Plate: L6B001 row: A column: 20.
Location/Qualifiers
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Allard,F., Crosby,W.L., Danyluk,J., Eudes,F., Fr Genswein,B., Graf,R., Gulick,P., Hrycan,L.D., La Links,M.G., McCarthy,E.L., Monroy,A., Muzak,I., Penniket,C., Roach,J.L. and Sarhan,F.
Functional Genomics of Abiotic Stress In Wheat a Unpublished (2003)
Contact: Wm L Crosby
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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               /organism="Triticum aestivum"
/mol_type="mRNA"
/db_xref="taxon:4565"
/clone_lib="Triticum aestivum FGAS: Library 6 CAP GATE 1"
/note="Organ: Crown and leaf; Vector: pCMV.SPORT6; Crown
(50%) and leaf (50%) tissues from wheat cultivar Norstar after
after short exposure times to low temperature in the light and in the dark. 12 mRNA populations were combined before constructing the library. The first 6 populations: After 7
days of growth at 20, wheat plants were transferred to 4C in the light. 1cm crown sections and green leaf tissu were separately harvested after 1, 3, and 6 hours of low temperature exposure. The last 6 populations: After 7 days of growth at 20C, wheat plants were transferred to 4C in the dark. 1cm crown sections and green leaf tissu were separately harvested after 1, 3, and 6 hours of low temperature exposure. First strand synthesis in this library was done in the presence of methylated dCTP thereby protecting from internal cleavage with Not1. In addition, this library used a primer for second strand synthesis that annealed to an artificial sequence (RNA sequences from EST generated from this library will be measted for vector and adaptor and additional sequence and additional sequenc
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Laroche, A.
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                                                              Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.

1 (bases 1 to 1064)
Allard, F., Crosby, W.L., Danyluk, J., Eudes, F., Frick, M., Gaudet, D.,
Genswein, B., Graf, R., Gulick, P., Hrycan, L.D., Laroche, A.,
Links, M.G., McCarthy, E.L., Monroy, A., Muzak, I., Nilson, D.,
Penniket, C., Roach, J.L. and Sarhan, F.
Functional Genomics of Abiotic Stress In Wheat and Canola Crops
                                                                                                                                                                                                                                                                             aestivum cDNA, mRNA seqn
CK163121
CK163121.1 GI:38993028
Unpublished (2003)
Contact: Wm L Crosby
Bioinformatics
University of Saskatchewan,
                                                                                                                                                                                                                                                                                                               1064 FGAS015739 Triticum aestivum aestivum cDNA, mRNA sequence.
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48.1%;
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Saskatchewan, S7N 5
Tel: 306 966 1769
Fax: 306 966 2033
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This sequence is the direct result of the Base calling softwa
Phred (default parameters). It is the raw base calls. To aid
identification of the high quality insert the software Lucy
(default parameters) has been run on this sequence. Lucy iden
the region [1,834].
GACGGCAAGGTGAGCCAGAACTACCCCATCGTGCAGAACCTGCAGGGCCAGATGGTGCAC
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/mol_type="mRNA"
/db_xref="taxon:4565"
/clone_lib="Triticum aestivum FGAS: Library 4 Gate 8"
/clone_lib="Triticum aestivum FGA
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Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
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Other_GSSs: OG3AG53TV
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                      GGAGGAGAGATGCGCGGCCTGCTGCGCGTGCTGCGGGCCA---AGGACGAGCAGGAGTA
                                                        GTACAGCCCCGTGAGCATCCTGGACATCCGCCAAGGCCCCTAAGGAGCCCTTCCGCGACTA
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/clone_lib="ZM_0.7_1.5_KB"
/note="Vector: pBCSK-; Site_1: HincII; 0."
methylation filtered genomic DNA library"
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/db_xref="taxon:4577"
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                                                                                                                                                              University of Saskatchewan, Department of Computer Science 1C101 Engineering Building, 57 Campus Drive, Saskatoon, Saskatchewan, S7N 5A9, Canada Tel: 306 966 1769 Fax: 306 966 2033 Email: fgas_ests@cs.usask.ca
This sequence is the direct result of the Base calling software Phred (default parameters). It is the raw base calls. To aid in identification of the high quality insert the software Lucy (default parameters) has been run on this sequence. Lucy identithe region [8,827].

Plate: L4B008 row: F column: 04.
Location/Qualifiers
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1 (bases 1 to 1138)

1 (bases 1 to 1138)

Allard,F., Crosby,W.L., Danyluk,J., Eudes,F., Frick,M., Gaudet,I Genswein,B., Graf,R., Gulick,P., Hrycan,L.D., Laroche,A., Links,M.G., McCarthy,E.L., Monroy,A., Muzak,I., Nilson,D., Penniket,C., Roach,J.L. and Sarhan,F.

Functional Genomics of Abiotic Stress In Wheat and Canola Crops Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                            Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Wm L Crosby
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CK163513 1138 FGAS016142 Triticum aestivum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCAGGAGACATCGAGGCGCGCGCTGGGCGAGCCCCGACGTGGAGCGCCGGGAGAACGGGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GATGCAGAAGAGCAACTTCAAGGGCCCCCGGCGCAACGTCAAGTGCTTCAACTGCGGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTCCGGCGCCGTGACGTGCGGCGCGCGCGCGCGCCGCGTCAACACGGTGGAGCACGG
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/mol type="mRNA"
/db_xref="taxon:4565"
/db_xref="taxon:4565"
/clone_lib="Triticum aestivum FGAS: Library 4 Gate 8'
/clone_lib="Triticum aestivum FGAS: Library 4 Gate 8'
/note="Organ: Crown and leaf; Vector: pCMV.SPORT6;
Conditions for growth: Seeds were germinated in a
water-saturated mix (50% black earth and 50% ProMix)
growth chamber for 7 days under an irradiance of 200
                                                                                                                              organism="Triticum aestivum"
                                                                                                                                                   1. .1138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mRNA sequence.
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4 Gate
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EST 05-DE

Gaudet, D.,

05-DEC-2003

software

identified aid in the

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m-2 sec-1. The temperature was maintained at 20 degrees C with a 15-hr photoperiod under a relative humidity of 70%. After this period watering of plants was stopped. Four time points were sampled during a two week period; the first after wilting was observed and the last, two weeks later, consisted of live crown and leaf tissue (leaf tissue that was yellow was not included in sampled material). First strand synthesis in this library was done in the presence of methylated dCTP thereby protecting from internal cleavage with NotI."
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ঠ 🔓 ঠ В S 5 ঠ 멍 В ঠ 멍 र् 8 δ 밁 밁 Query Match Best Local Similarity Matches 283; Conserv 592 484 532 472 662 709 649 544 424 412 304 352 124 GAGGGCTTCGCCCTGAACCCCCGGCCTGCTGGAGACCGCCGAGGGCTGCAAGCAGATCATG 183 769 604 ATCAACGAGGAGGCCGCCGAGTGGGACCGCCTGCACCCCGTGCAGGCCGGC--CCCGTGG 364 GACGGCAAGGTGAGCCAGAACTACCCCCATCGTGCAGAACCTGCAGGGCCCAGATGGTGCAC 423 244 292 184 AAGCAGCTGCAGCCCGCCCTGCAGACCGGCACCGAGGAGCTGCGCAGCCTGTACAACACC CCCCCGGCCAGATGCGCGACCCCCGCGGCAGCAGCGACATCGCCGGCGCGACCACCA 712 AGATCTGCCAGCTCCCCGTCGGCGACGGCATCACCCTCTGCCGCCGCGCCCA 819 CGCTACTACCGCGACTTCGTCCTCGAGCTCAACAGGCCCTCGCCGNCGACCAGCGCGTCG AACACGATGTTGAACACCGTGGGCGGCCACCAGGCCGCCATGCAGATGCTGAAGGACACCC AACTACCACGAGCGCCTCATGAAGCTCGTCAAGGTCGGCGGCCTCCTCGGCTACGAC---GAGGCCAACCACGGGACCTTCGACTTCGTCTTCGTGGACGCCGACAAGGACAACTACCTC CAGGCCATCAGCCCCGCACCCTGAACGCCTGGGTGAAGGTGATCGAGGAGAAGGCCTTC CACAAGATCGACTTCCGCGAGGGCCCGGCGCTGCCCGTCCTGGACGCCTGCTGGAGGAC GACAAGATCGAGGAGGAGCAGAACAAGTCCCAGCAGAAGACCCAGCAGGCCAAGGAGGCC 363 GTGGCCACCCTGTACTGCGTGCACGCCGGCATCGAGGTCCGCGACACCAAGGAGGCCCTG CTCAACATGCTGCTCAAGCTCATCGGCGCCAAGAAGACCATGGAGATCGGCGTCTACACC GAGATCACCGCCAACCACCCATGGAACCTGATGACGACGTCGGCGGACGAGGGCCAGTTC 291 GACATCAACCGCGAGAACTACGAGCTGGGGCTGCCGTGCATCGAGAAGGCCGGCGTGGCG GGCTACTCCCTGCTCGCCACCGCGCTCGCCATCCCCGACGACGGCACCATCTTGGCCATG AACACCCTCTGGAACGGCTCCGTCGTGCTCCCCGCCGACGCCCCATGCGCAAGTACATC 5.1%; Score 76.8; DB 7; Length 1138; ilarity 47.9%; Pred. No. 0.00074; Conservative 0; Mismatches 303; Indels 5 <u>5</u> 768 661 708 603 648 543 591 483 531 471 411 303 351 243

Search completed: March 13, 2005, 00:13:49 Job time : 5318.82 secs

Oldsn) XNW TO FOX SIAL

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Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp
-Q=/cgn2 1/USPTO_spool_p/US09475704/runat 10032005 140222 14839/app query.fasta_1.3342
-DB=PIR 79 -QFMT=fastan -SUFFIX=n2p.rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09475704 @CGN 1 1 160 @runat 10032005 140222 14839 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Perfect score:
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Maximum Match 10
Listing first 45
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## ALIGNMENTS

RESULT 1

FOLIMD

gag polyprotein - human immunodeficiency virus type 1 (isolate NDK)

yAlternate names: core polyprotein

N;Contains: core protein p15; core protein p17; core protein p24

C;Species: human immunodeficiency virus type 1, HIV-1

A;Note: host Homo sapiens (man)

C;Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 09-Jul-2004

C;Accession: J00065

R;Spire, B; Sire, J; Zachar, V:, Rey, F:; Barre-Sinoussi, F:; Galibert, F:; Hampe, A:;
Gene 81, 275-284, 1989

A;Title: Nucleotide sequence of HIVI-NDK: a highly cytopathic strain of the human immuno

A;Reference number: J00065; MUID:90034200; PMID:2806917

A;Residues: 1-497 <SPI:

A;Residues: 1-497 <SPI:

A;Cross-references: UNIPROT:P18800; GB:M27323; NID:g328154; PIDN:AAA44868.1; PID:g328157

C;Genetics:
A;Gene: gag
C;Superfamily: AIDS-related virus gag polyprotein
C;Keywords: AIDS; core protein p17 #status predicted <C24>
F;130-189/Product: core protein p17 #status predicted <C15>

Alignment Scores:
1.82e-106

Percent Similarity: 91.49%
Percent Similarity: 91.49%
Percent Similarity: 93.76%
Query Matches: 32

Query Match: 1

DB: 103-475-704A-4 (1-1509) x FOLJND (1-497)

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                        GCCGAGGCGATGAGCCAG-----GCCAACAGCGTGAACATCATGATGCAGAAAGAGCAAC
                                                      GluGluMetMetThrAlaCysGlnGlyValGlyGlyProGlyHisLysAlaArgValLeu
                                                                                                                  GlnAsnAlaAsnProAspCysLysThrIleLeuLysAlaLeuGlyProGlnAlaThrLeu
                                                                                                                               CAGAACGCCAACCCCGACTGCAAGACCATCCTGCGCGCTCTCGGCCCCGGCGCCACCCTG
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| IleGlyGlnLeuG
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A; Molecule type: DNA
A; Residues: 1-502 <SAN>
A; Residues: 1-502 <SAN>
A; Residues: 1-502 <SAN>
A; Cross-references: UNIPROT: P03349; GB: K02007; NID: g328658; PIDN: AAB59875.1; PID: g328661
C; Comment: Cleavage sites that yield the mature core proteins remain to be determined.
C; Genetics:
A; Gene: gag
C; Superfamily: AIDS-related virus gag polyprotein
C; Keywords: AIDS; core protein; immunodeficiency; polyprotein
F;1-134/Product: core protein p17 #status predicted <P17>
F;135-393/Product: core protein p24 #status predicted <P24>
F;394-502/Product: core protein p15 #status predicted <P15>
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Science 227, 484-492, 1985
A;Title: Nucleotide sequence and expression
A;Reference number: A04003; MUID:85090453; F
A;Accession: A03947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gag polyprotein - human immunodeficiency virus type 1 (isolate ARV-2)
N;Alternate names: core polyprotein
N;Contains: core protein p15; core protein p17; core protein p24
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 09-Jul-2004
C;Accession: A03947
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Query Match:
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Indels:
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                                                  CAGAAGAGCAACTTCAAGGGCCCCCCGGCGCAACGTCAAGTGCTTCAACTGCGGCAAGGAG
                                                                                                                       LysAlaArgValLeuAlaGluAlaMetSerGlnValThrAsnProAlaAsnIleMetMet
                                                                                                                                                         AAGGCCCGCGTGCTGGCCGAGGCGATGAGCCAG---GCCAACAGCGTGAACATCATGATG
                                                                                                                                                                                            ProAlaAlaThrLeuGluGluMetMetThrAlaCysGlnGlyValGlyGlyProGlyHis
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C;Superfamil
C;Keywords:
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C;Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change
C;Accession: A03945
R;Ratner, L.; Haseltine, W.; Patarca, R.; Livak, K.J.; Starcich, nberger, J.A.; Papas, T.S.; Ghrayeb, J.; Chang, N.T.; Gallo, R.C Nature 313, 277-284, 1985
A;Title: Complete nucleotide sequence of the AIDS virus, HTLV-II A;Reference number: A93353; MUID:85111123; PMID:2578615
A;Accession: A03945
A;Accession: A03945
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Best Local Similarity:
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DB:
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A;Residues: 1-512 <RAT>
A;Residues: 1-512 <RAT>
A;Residues: 1-512 <RAT>
C;Cross-references: UNIPROT:P03347; GB:M15654; GB:K02008; GB:K02009; GB:K02010; NID:g326
C;Comment: Cleavage sites that yield the mature core proteins remain to be determined.
C;Genetics:
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Query
DB:
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C;Superfamily: AIDS-related virus gag polyprotein
C;Keywords: core protein; polyprotein
C;Keywords: core protein p17 #status predicted
F;1-132/Product: core protein p24 #status predicte
F;133-391/Product: core protein p15 #status predicte
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FOVWH4
FOVWH4
gag polyprotein - human immunodeficiency virus type 1 (isolate CDC-451)
N;Alternate names: core polyprotein
N;Contains: core protein p15; core protein p17; core protein p24
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
C;Accession: A25523
C;Accession: A25523
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A;Title: Molecular cloning and primary nucleotide sequence & A;Reference number: A94136; MUID:87041461; PMID:3490666
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|YArgProGlyAsnPheLeuGlnSerArgProGl
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ACCCCCCAGGACCTGAACACGATGTTGAACACCGTGGGCCGCCACCCAGGCCGCCATGCAG

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RESULT 5
$54377

gag polyprotein - human immunodeficiency virus type 1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Species: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_C;Accession: S54377
R;Theodore, T.; Buckler-White, A.J.
submitted to the EMBL Data Library, July 1989
A;Reference number: S54377
A;Accession: S54377
A;Status: preliminary
A;Molecule type: genomic RNA
A;Residues: 1-501 <THE>
A;Cross-references: UNIPROT:P12495; EMBL:M22639; NID:g32-C;Superfamily: AIDS-related virus gag polyprotein
C;Keywords: polyprotein
                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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|AlaAspAlaGlyAsnAsnSerGlnValSerGlnAsnTyr
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90.37%
83.30%
78.61%
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Conservative:
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05-Dec-1998

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RESULT 6
FOUWLV
gag polyprotein - human immunodeficiency virus type 1 (isolate LAV-1a)
N;Alternate names: assemblin; core polyprotein; gag precursor
N;Contains: capsid antigen core protein p24CA; core protein p1; core p
C;Species: human immunodeficiency virus type 1, HIV-1
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LeuPheGlyAsnAspProLeuLeuGln
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A;Gene: gag
C;Superfamily: AIDS-related virus gag polyprotein
C;Keywords: AIDS; blocked amino end; core protein; immunodeficiency; l
F;2-500/Product: gag precursor (assemblin) #status predicted <GAG>
F;2-132/Product: matrix antigen core protein pl7MA #status predicted <
F;20-32/Region: nuclear location signal
F;110-114/Region: nuclear location signal
F;133-363/Product: core protein p2 #status predicted <CP2>
F;378-432/Product: nucleocapsid core protein p7NC #status predicted
F;364-377/Product: nucleocapsid core protein p7NC #status predicted <CP2>
F;378-432/Product: nucleocapsid core protein p7NC #status predicted <CP;392-405/Region: zinc finger CCHC motif
F;413-426/Region: zinc finger CCHC motif
F;433-448/Product: core protein p1 #status predicted <CP1>
F;449-500/Product: core protein p6 #status predicted <CP6>
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status expe
F;413,416,421,426/Binding site: zinc (Cys, Cys, His, Cys) #status expe
                                                                                                                                                                                                                                                                                                                                             Score:
Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Note: host Homo sapiens (man)
C;Date: 17-May-1985 #sequence_revision 17
C;Accession: A03946
R;Wain-Hobson, S.; Sonigo, P.; Danos, O.;
Cell 40, 9-17, 1985
A;Title: Nucleotide sequence of the AIDS 1
A;Reference number: A90866; MUID:85099333
A;Accession: A03946
A;Molecule type: DNA
A;Residues: 1-500 <WAI>
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LeuGlyGlnLeuGl
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90.55%
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Conservative:
Mismatches:
Indels:
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                                                                                                                     ProThrAlaProProGluGluSerPheArgSerGlyValGluThrThrThrProSerGln
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   human
immunodeficiency virus type
  (strain
  YU-2)
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A;Residues: 1-500 <LIY>
A;Residues: 1-500 <LIY>
A;Cross-references: UNIPROT:P35962; GB:M93258
C;Genetics:
A;Gene: gag
C;Superfamily: AIDS-related virus gag polyprotein
C;Keywords: AIDS; core protein; immunodeficiency; polyprotein
C;Keywords: AIDS; core protein p17 #status predicted <P17>
F;1-132/Product: core protein p24 #status predicted <P24>
F;392-500/Product: core protein p15 #status predicted <P15>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N;Alternate names: core polyprotein
N;Contains: core protein p15; core protein p17; core protein
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_chan
C;Accession: A44001
C;Accession: A44001
C;Accession: A6, 6587-6600, 1992
A;Title: Complete nucleotide sequence, genome organization, a
A;Reference number: A44001; MUID:93021387; PMID:1404605
A;Accession: A44001
A;Molocula tropa
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:Q78240; EMBL:Z11530; NID:g60192; virus gag polyprotein

PIDN: CAA77621.1;

PID:g60193

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RESULT 8
$33979
gag polyprotein - human immunodeficiency virus type 1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #te
C;Accession: $33979
R;Carlini, F.
submitted to the EMBL Data Library, November 1991
A;Reference number: $33979
A;Accession: $33979
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A;Molecule type: mRNA
A;Residues: 1-500 <CAR>
A;Cross-references: UNIPROT:Q
C;Superfamily: AIDS-related v
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Alignment Scores:  4.78e-104	A;Status: prediminary; translated from GB/EMBL/DDBJ A;Status: prediminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-505 <ali> A;Cross-references: UNIPROT:P04594; EMBL:K03456; NID:g60228; PIDN:CAA28011.1; PID:g60229 A;Cross-references: UNIPROT:P04594; EMBL:K03456; NID:g60228; PIDN:CAA28011.1; PID:g60229 C;Superfamily: AIDS-related virus gag polyprotein</ali>	C;Accession: T01667 R;Alizon, M.; Wain-Hobson, S.; Gluckman, J.C.; Sonigo, P. Cell 46, 63-74, 1986 A;Title: Genetic variability of the AIDS virus: Nucleotide sequence analysis of two isol A;Reference rumber: Z14389; MUID:86245056; PMID:2424612	RESULT 9 T01667 T01667 gag polyprotein - human immunodeficiency virus type 1 C;Species: human immunodeficiency virus type 1, HIV-1 C;Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 09-Jul-2004	Qy 1483 TTCGGCAGCGGCCCCTGAGCCAG 1506       :::           Db 493 PheGlyAsnAspProSerSerGln 500	Qy 1423 AAGCAGGAGCCCAAGGACCGCGAGCCCTACCGCGAGCCCTGACCGCCAGCCTG 1482	Qy 1369 CCCACCGCCCCCCCCCGCCGAGAGCTTCCGCTTCGAGGAGACCACCCCCGCCCCC 1422	QY 1309 CACAAGGGCCGCCCGGCAACTTCCTGCAGAACCGCAGCGAGCCCGCCGCCCCCCCC	Qy 1249 CACCAGATGAAGGACTGCACCGAGCGCCAGGCCAACCTTCCTGGGCAAGATCTGGCCCAGC 1308	Qy 1189 ATCGCCAAGAACTGCCGCCCCCCCCCCAAGAAGGGCTGCTGGAAGTGCCGCAAGGAGGGC 1248        :::	Qy 1129 AGCAACTTCAAAGGGCCCCCCGGCGCAACGTCAAGTGCTTCAACTGCĞGCAAGGAGGGCCAC 1188    :::	Qy 1072 CGCGTGCTGGCCGAGGCGATGAGCCAGGCCAACAGCGTGAACATCATGATGCAGAAG 1128	Qy 1012 GCCACCCTGGAGGAGATGATGATGACCGCCTGCCAGGGCGTGGGCGGCCCCGGCCACAAGGCC 1071	Qy       952       CTGCTGGTGCAGAACGCCAACCCCGACTGCAAGACCATCCTGCGGCGCTCTCGGGCCCCGGC       1011	Qy 892 TTCAAGACCCTGCGCGCGCGAGCAGGCCACCCAGGACGTGAAGAACTGGATGACCGAGACC 951 :::	
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34 AACTGGATGACCGAGACCCTGCTGGTGCAGAACGCCAACCCCGACTGCAAGACCCATCCTG	281 ArgMetTyrSerProValSerIleLeuAspIleArgGlnGlyProLysGluProPheArg 300  874 GACTACGTGGACCGCTTCTTCAAGACCCTGCGCGCGAGGACCCCAGGACGTGAAG 933  871 ArgMetTyrSerProValSerIleLeuAspIleArgGlnGlyProLysGluProPheArg 300  872 GACTACGTGGACCGCTTCTTCAAGACCCTGCGCGCCGAGGACCCCAGGACGTGAAG 933  873 GACTACGTGAACCGCTTCTTCAAGACCCTGCGCGCCGAGGCAGGC	54 CCCGTGCCCGTGGGCGACATCTACAAGCGGTGGATCATCCTGGGCCTGAACAAGATCGTG    :::	alHisProvalHisAlaGlyProIleProProGlyGlnMetArgGluProArgGl ACATCGCCGGCGCCAGCAGCACCCTGCAGGAGCAGATCGCCTGGATGACCAGCAF 	inalaAlaMetGinMetLeuLysAspThrileAsnGluGluAlaAlaAspTrpAs TGCACCCCGTGCAGGCCCGGCCCCGTGGCCCCCGGCCAGATGCGCGACCCCCGCGG ::	SerGluGlyAlaThrProGlnAspLeuAsnMetMetLeuAsnIleValGlyGl GCCGCCATGCAGATGCTGAAGGACACCATCAACGAGGAGGCCGCCGAGTGGGA 	allysValIleGluGluLysAlaPheSerProGluValIleProMetPheSe GCGAGGGCGCCACCCCCAGGACCTGAACACGATGTTGAACACCGTGGGCGC	alGlnAsnAlaGlnGlyGlnMetIleHisGlnAlaIleSerProArgThrLeuAk GGGTGAAGGTGATCGAGGAGAAGGCCTTCAGCCCCGAGGTGATCCCCATGTTCAC	lnGlnAlaAlaAlaThrLysAsnSerSerSerValSerGlnAsnTyrPı hGAACCTGCAGGGCCAGATGGTGCACCAGGCCATCAGCCCCGCACCCTGAI	euAspLysIleGluGluIleGlnAsnLysSerArgGlnLysThrGlnGlnA CCGACGGCAAGGTGAGCCAGAACT	hrValAlaThrLeuTyrCysValHisGlnArgIleAspValLysAspThrLysGl TGGACAAGATCGAGGAGGAGCAGAACAAGTCCCAGCAGAAGACCCAGCAGCCAG	luglnLeuglnSerThrLeuLysThrGlySerGluGluIleLysSerLeuT luglnLeuGlnSerThrLeuLysThrGlySerGluGluIleLysSerLeuT TGGCCACCCTGTACTGCGTGCACGCCGGCATCGAGGTCCGCGACACCAAGG	LeuGluArgPheAlaLeuAsnProGlyLeuLeuGluThrGlyGluGlyCysGlnGl ATGAAGCAGCTGCAGCCCGCCCTGCAGACCGGCACCGAGGAGCTGCGCAGCCTGT#	LeuArgProGlyGlyLysLysLysTyrArgLeuLysHisLeuValTrpAlaSerAr CTGGAGGGCTTCGCCCTGAACCCCGGCCTGCTGGAGACCGCCGAGGGCTGCAAGCA	1 MetGlyAlaArgAlaSerValLeuSerGlyGlyLysLeuAspAlaTrpGluLysileArg 20 61 CTGCGCCCCGGCGCAAGAAGCACTACATGCTGAAGCACCTGGTGTGGGCCAGCCGCGAG 120	1 ATGGGCGCCCGCGCAGCATCCTGCGCGGCGAGAAGCTGGACAAGTGGGAGAAGATCCGC 60

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gag polyprotein - human immunodeficiency virus type 1 (strain JRFL) C; Species: human immunodeficiency virus type 1, HIV-1 C; Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004 C; Accession: T09436 R; Pang, S.; Vinters, H.V.; Akashi, T.; O'Brien, W.A.; Chen, I.S.; Koyanagi, submitted to the EMBL Data Library, July 1996 A; Reference number: Z16673 A; Accession: T09436 A; Status: preliminary; translated from GB/EMBL/DDBJ A: Molecule type: DNA
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A; Residues: 1-498 < PAN>
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                                                             PheArgAsnGlnArgLysIleValLysCysPheAsnCysGlyLysGluGlyHisIleAla
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A;Gene: gag
C;Superfamily: AIDS-related virus gag polyprotein
C;Keywords: AIDS; core protein; immunodeficiency; polyprotein
F;1-134/Product: core protein p17 #status experimental <P17>
F;135-365/Product: core protein p24 #status experimental <P24>
F;366-379/Product: core protein p2 #status experimental <PP2>
F;380-434/Product: core protein p7 #status experimental <PP7>
F;435-450/Product: core protein p1 #status experimental <PP1>
F;435-450/Product: core protein p6 #status experimental <PP6>
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A38068
gag polyprotein - human immunodeficiency virus type 1 (strain MN)
N;Alternate names: core polyprotein
N;Contains: core protein pl; core protein pl7; core protein p2; core protein p24; core p
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: A38068
R;Henderson, L.E.; Bowers, M.A.; Sowder II, R.C.; Serabyn, S.A.; Johnson, D.G.; Bess Jr.
J. Virol. 66, 1856-1865, 1992
A;Title: Gag proteins of the highly replicative MN strain of human immunodeficiency viru A;Reference number: A38068; MUID:92194415; PMID:1548743
A;Accession: A38068
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A; Residues: 1-506 < HEN>
A; Cross-references: UNIPROT: P05888
C; Genetics:
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•	Qy 181 ATGAAGCAGCTGCAGCCCGCCCTGCAGACCGGCACCGAGGAGCTGCGCAGCCTGTACAAC 240 :::	QY 121 CTGGAGGGCTTCGCCCTGAACCCCGGCCTGCTGGAGACCGCCGAGGGCCTGCAAGCAGATC 180	Qy 61 CTGCGCCCCGGCGGCAAGAAGCACTACATGCTGAAGCACCTGGTGTGGGCCAGCCGCGAG 120	Qy 1 ATGGGCCCGCCGCCAGCATCCTGCGCGGCGAGAAGCTGGACAAGTGGGAGAAGATCCGC 60	1tch: 71.07% Indels: 1 Gaps: 5 5-704A-4 (1-1509) x FOVWVL (1-478)	Pred. No.: 1.15e-94 Length: 478 Score: 2018.50 Matches: 382 Percent Similarity: 87.86% Conservative: 45 Best Local Similarity: 78.60% Mismatches: 40	00,405/Binding site: zinc (Cys, Cys, His, Cys) #status experimental 21,426/Binding site: zinc (Cys, Cys, His, Cys) #status experimental cores:	egion: zinc finger CCHC motif egion: zinc finger CCHC motif d site: myristylated amino end (Gly) (in mature form) #status	egion: nuclear location signal roduct: capsid antigen core protein p24CA #status predicte roduct: core protein p2 #status predicted <cp2></cp2>	C; superiamily: AIDS-related virus gag polyprotein C; Keywords: AIDS; blocked amino end; core protein; immunodeficiency; lipoprotein; myrist F; 2-478/Product: gag precursor (assemblin) #status predicted <gag> F; 2-132/Product: matrix antigen core protein p17MA #status predicted <p17> F; 20-32/Region: nuclear location signal</p17></gag>	erences: UNIPROT: P03350	A;Reference number: A93355; MUID:85111157; PMID:2982104 A;Reference number: A93355; MUID:85111157; PMID:2982104 A;Recession: A03948 A;Molecule type: DNA A;Molecule type: DNA	: A03948  M.A.; Smith, D.H.; Cabradilla, C.D.; Benton, C.V.; Lasky, L.A.; Capon, D.J. 450-458, 1985	939 polyprotein - human immunodeficiency virus type 1 (isolate LV) N;Alternate names: assemblin; core polyprotein; gag precursor N;Contains: capsid antigen core protein p24CA; core protein p1; core protein p6; matrix C;Species: human immunodeficiency virus type 1, HIV-1 C;Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 09-Jul-2004	To the second of	QY 1465 ACCGCCCTGCGCAGCCTGTTCGGCAGCCGCCCCTGAGCCAG 1506  :::   :::	QY 1417 GCCCCCAAGCAGGAGCCCAAGGACCGCGAGCCCTACCGCGAGCCCCTG 1464	457ProThrAlaProProGluGluSerPheArgPheGlyGluGluT	441 ProSerCysLysGlyArgProGlyAsnPheProGlnSerArgThrGlu 456
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R;Huet, T.; Cheynier, R.; Meyerhans, A.; Roelants, G.; Wain-Hobson, S.
Nature 345, 356-359, 1990
A;Title: Genetic organization of a chimpanzee lentivirus related to HIV-1.
A;Reference number: S09983; MUID:90259077; PMID:2188136
A;Accession: S09983
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-508 <HUE>
A;Cross-references: UNIPROT:P17282; EMBL:X52154; NID:g58866; PIDN:CAA36401
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C;Superfamily: AIDS-related virus
C;Keywords: AIDS; core protein; in
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C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: S09983
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ThrArgGluGlyGlnGlyIlePhePheArgAlaAspGlnSerGln--
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                                                                                                                    ThrLeuAlaValLeuTrpCysIleHisSerAspIleThrValGluAspThrGlnLysAla
                                 SerArgGluGlyGlyAlaSerGlnGlyAlaSerAlaSerAlaGlyIleSerGlyAsnT
                                                                         -----GlnProHisHisPhePheArgAlaAspGlnSer----
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           CCCCTGACCGCCCTGCGCAGCCTGTTCGGCAGCGGCCCCCCTGAGCCAG
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                                           TyrGlnGluGluLysSer-----GlnGluLysLysGluGlyGluSerSerLeuTyr
                                                                TTCGAGGAGACCACCCCCGCCCCAAGCAGGAGCCCAAGGACCGCGAGCCCTACCGCGAG 1458
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756

257

699 218 639

237

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gag polyprotein - simian immunodeficiency virus (strain stm)
N;Alternate names: core polyprotein
N;Contains: core protein p17; core protein p24
C;Species: simian immunodeficiency virus, SIV
A;Note: host Macaca arctoides (stump-tailed macaque)
C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 09-Jul-2004
C;Accession: A41565
R;Khan, A.S.; Galvin, T.A.; Lowenstine, L.J.; Jennings, M.B.; Gardner, M.B.;
J. Virol. 65, 7061-7065, 1991
A;Title: A highly divergent simian immunodeficiency virus (SIVstm) recovered
A;Reference number: A41565; MUID:92046379; PMID:1942258
A;Accession: A41565
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Query
DB:
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A;Residues: 1-510 <KHA>
A;Cross-references: UNIPROT:P31634; GB:X60667; NID:g60527;
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Superfamily: AIDS-related virus gag polyprotein
C;Keywords: core protein; polyprotein
F;1-115/Product: core protein p17 #status predicted <P17>
F;116-510/Product: core protein p24 #status predicted <P2
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                                                                       AAGGTGATCGAGGAGAAGGCCTTCAGCCCCGAGGTGATCCCCATGTTCACCGCCCTGAGC
                                                                                                                                             ThrSerArgProThrAlaProProSerGlyArg---GlyGlyAsnTyrPro---ValGln
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                                                                                                                                                                                                                                                                                                                                                                               AAGGAGGGCCACATCGCCAAGAACTGCCGCGCCCCCCCAAGAAGGGGCTGCTGGAAGTGC
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| ProGlyGlnLysAlaArgLeuMetAlaGluAlaLeuLysGluAlaPheGlnProGlyPro
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                         2005,
                         15:43:51
                                                                                                                                  -GAGCCCCTGACCGCCCTGCGCAGC
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1056 337 936 297 876 277 816

377 1116

417

COLAGON ANNA BELEVA SIALL

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Score

Match

Length

BG

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Description

US-09-899-575-17 US-10-332-413-2

2606 2448 2435 2435 2435 2415. 2407. 2407. 260.

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Command line parameters:
-MODEL=frame+ n2p.model -DEV=xlp
-Q=/cgn2 1/USPTO_spool_p/US09475704/runat_10032005_140224_14937/app_query.fasta_1.3342
-DB=PublIshed_Applications_AA -QFMT=fastan -SUFFIX=n2p.rapb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09475704 @CGN 1 1 466 @runat 10032005 140224 14937
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPOEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Pred. No. is the number of results predicted by chance to hav score greater than or equal to the score of the result being and is derived by analysis of the total score distribution.
                                                                                                                                      Published_Applications_AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

15: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

17: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*

19: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

19: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Sequence 17, Appl Sequence 2, Appli Sequence 5, Appli Sequence 110, App Sequence 110, App Sequence 109, App Sequence 104, App Sequence 104, App Sequence 106, App Sequence 106, App Sequence 107, App Sequence 120, App Sequence 126, App Sequence 22, Appli Sequence 27, Appli Sequence 26, Appli Sequence 27, Appli Sequence 27, Appli Sequence 26, Appli Sequence 27, Appli Sequence 26, Appli Sequence 27, Appli Sequence 27, Appli Sequence 28, Appli Sequence 27, Appli Sequence 27, Appli Sequence 28, Appli Sequence 27, Appli Sequence 136, Appli Sequence 136, Appli Sequence 137, Appli Sequence 111, Appli Sequence 111, Appli Sequence 111, Appli Sequence 111, Appli Sequence 31, Appli Sequence 32, A

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6 US-10-332-413-8
4 US-10-339-217-110
9 US-10-339-217-109
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US-10-339-217-100

US-10-339-217-31

US-10-339-217-31

US-10-339-217-31

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US-10-339-217-32

US-10-339-217-32

US-10-339-217-32

ALIGNMENTS

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; SOFTWAKE: PACENCIN VET. 2.0 ; SEQ ID NO 17 ; LENGTH: 492 ; TYPE: PRT ; ORGANISM: Human immunodeficiency virus	; CURRENT FILING DATE: 2001-07-05 ; PRIOR APPLICATION NUMBER: 09/475,704 ; PRIOR FILING DATE: 1999-12-30 ; NUMBER OF DECITE US: 135	; APPLICANT: Egnelbrecht, Susan ; APPLICANT: van Rensburg, Estrelita Janse ; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C ; TITLE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF ; FILE REFERENCE: P01631.102 ; CURRENT APPLICATION NUMBER: US/09/899,575	RESULT 1  US-09-899-575-17  ; Sequence 17, Application US/09899575  ; Publication No. US20030223961A1  ; GENERAL INFORMATION:  ; APPLICANT: Zur Megede, Jan  ; APPLICANT: Barnett, Susan W.

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SUMMARIES

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Best Local Similarity:
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                      CTGGACATCAAGCAGGGCCCCAAGGAGCCCCTTCCGCGACTACGTGGACCGCTTCTTCAAG
                                           LysArgTrpIleIleLeuGlyLeuAsnLysIleValArgMetTyrSerProValSerIle
                                                                       ACCCTGCGCGCGAGCAGAGCACCCAGGAGGTGAAGAACTGGATGACCGACACCCTGCTG
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                                                        AAGCGGTGGATCATCCTGGGCCTGAACAAGATCGTGCGGATGTACAGCCCCCGTGAGCATC
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Conservative:
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Alignment Scores: Pred. No.: Score:
                           ; TYPE: PRT
; ORGANISM: Human
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APPLICANT: Morris, Lynn
APPLICANT: Karim, Salim Abdool
APPLICANT: Williamson, Carolyn
ITILE OF INVENTION: Process for the Selection of HIV-1 Subtype C Isolates, Selected H
ITILE OF INVENTION: Subtype Isolates, Their Genes nd Modifications and Derivatives T
FILE REFERENCE: 45669-281993
CURRENT APPLICATION NUMBER: US/10/332,413
CURRENT FILING DATE: 2003-09-12
PRIOR APPLICATION NUMBER: PCT/IBO1/01208
PRIOR FILING DATE: 2001-07-09
PRIOR FILING DATE: 2001-07-07
PRIOR APPLICATION NUMBER: US 60/216,995
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-09-15
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LEWING AGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/10332413; Publication No. US20040116660A1; GENERAL INFORMATION:
APPLICANT: Johnstone, Robert Edward; APPLICANT: Swanstrom, Ronald Ivar; APPLICANT: Morris, Lynn; APPLICANT: Karim, Salim Abdool; APPLICANT: Williamson, Carolyn
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US-09-991-258-5

; Sequence 5, Application US/09991258

; Patent No. US20020141975A1

; GENERAL INFORMATION:

; APPLICANT: Olmsted, Robert

APPLICANT: Caley, Ian

APPLICANT: Dryga, Sergey

APPLICANT: Davis, Nancy

APPLICANT: Davis, Nancy

APPLICANT: Davis, Nancy

APPLICANT: Davis, Nancy

APPLICANT: Swanstrom, Robert

APPLICANT: Swanstrom, Ronald

TITLE OF INVENTION: VACCINES

FILE REFERENCE: 01113.0001U3

CURRENT APPLICATION NUMBER: US/09/991,258

CURRENT FILING DATE: 2001-01-16

PRIOR APPLICATION NUMBER: 60/216,995

PRIOR APPLICATION NUMBER: 60/216,995

PRIOR FILING DATE: 2000-07-07

NUMBER OF SEQ ID NOS: 19

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 5

LENGTH: 492

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Bynthetic construct

US-09-991-258-5
Percent Similarity:
Best Local Similarity:
Query Match:
                                                            Alignment
Pred. No.:
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APPLICANT: Morris, Lynn
APPLICANT: Karim, Salim Abdool
APPLICANT: Williamson, Carolyn
TITLE OF INVENTION: Process for the Selection of HIV-1 Subtype C Isolates, Selected H
TITLE OF INVENTION: Subtype Isolates, Their Genes nd Modifications and Derivatives T
TITLE OF INVENTION Subtype Isolates, Their Genes nd Modifications and Derivatives T
CURRENT APPLICATION NUMBER: US/10/332,413
CURRENT FILING DATE: 2003-09-12
PRIOR APPLICATION NUMBER: PCT/IB01/01208
PRIOR APPLICATION NUMBER: US 60/216,995
PRIOR APPLICATION NUMBER: US 60/216,995
PRIOR APPLICATION NUMBER: ZA 2000/3437
PRIOR FILING DATE: 2000-07-10
PRIOR PILING DATE: 2000-07-10
PRIOR PILING DATE: Z000-09-15
NUMBER OF SEQ ID NOS: 32
CORTMADE: Detertion 1 1
                                                                                                                                                                          ; LENGTH: 631
; TYPE: PRT
; ORGANISM: Human i
US-10-332-413-8
                                   Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                      Alignment Scores: Pred. No.: Score:
US-09-475-704A-3 (1-1479) x US-10-332-413-8 (1-631)
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US-10-332-413-8
                                                                                                                                                                                                                                          SOFTWARE: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Johnstone, Robert Edward
APPLICANT: Swanstrom, Ronald Ivar
APPLICANT: Morris, Lynn
APPLICANT: Karim, Salim Abdool
APPLICANT: Williamson, Carolyn
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                     CTGGACATCAAGCAGGGCCCCAAGGAGCCCTTCCGCGACTACGTGGACCGCTTCTTCAAG
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Hou, Xiaohong

APPLICANT: Marlor, Christopher W.

APPLICANT: Marlor, Christopher W.

APPLICANT: Marlor, Christopher W.

APPLICANT: Marlor, Christopher W.

APPLICANT: Wang, Wengang

ITTLE OF INVENTION: Methods for Identifying Confile REFERENCE: 111021.143 (ACH-US1)

CURRENT APPLICATION NUMBER: US/10/339,217

CURRENT FILING DATE: 2003-01-09

PRIOR APPLICATION NUMBER: US 60/347,369

PRIOR PILING DATE: 2002-01-11

NUMBER OF SEQ ID NOS: 144

SOPTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 110

LENGTH: 492

TYPE: DET
                                                                                                                                                  Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: HIV-1
                                                                                                                                                                                            No.:
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         CTGGAGAAGTTCGCCCTGAACCCCGGCCTGCTGGAGACCAGCGAGGGCTGCAAGCAGATC
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CGCTTCGAGGAGACCACCCCCGGCCAGAAGCAGGAGCAAGGACCGGGAGACCCTGACC
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                                                               AAGGGCCCCCGGCATCGTCAAGTGCTTCAACTGCGGCAAGGAGGGCCACATCGCCCGC
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TITLE OF INVENTION: Methods for Identifying Compounds Which Inhibit Binding;
TITLE OF INVENTION: Nucleocapsid 7 Protein to HIV-1 RNA
FILE REFERENCE: 111021.143(ACH-US1)
CURRENT APPLICATION NUMBER: US/10/339,217
CURRENT FILING DATE: 2003-01-09
PRIOR APPLICATION NUMBER: US 60/347,369
PRIOR APPLICATION UMBER: US 60/347,369
PRIOR FILING DATE: 2002-01-11
NUMBER OF SEQ ID NOS: 144
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 109
LENGTH: 492
TYPE: PRT
ORGANISM: HIV-1
US-10-339-217-109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 109, Application US/10339;
Publication No. US20030198648A1
GENERAL INFORMATION:
APPLICANT: Buechter, Douglas
APPLICANT: Hou, Xiaohong
APPLICANT: Marlor, Christopher W.
APPLICANT: Rice, William G.
APPLICANT: Yang, Wengang
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p. US20030198648A1
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Sequence 140, Application US/10339217

Publication No. US20030198648A1

GENERAL INFORMATION:

APPLICANT: Buechter, Douglas

APPLICANT: Hou, Xiaohong

APPLICANT: Marlor, Christopher W.

APPLICANT: Rice, William G.

APPLICANT: Yang, Wengang

TITLE OF INVENTION: Nucleocapsid 7 Protein to

FILE REFERENCE: 111021.143(ACH-US1)

CURRENT APPLICATION NUMBER: US/10/339,217

CURRENT APPLICATION NUMBER: US/0/347,369

PRIOR APPLICATION NUMBER: US 60/347,369

PRIOR FILING DATE: 2002-01-11

NUMBER OF SEQ ID NOS: 144
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US-10-339-217-140
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Conservative:
Mismatches:
Indels:
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RESULT 8
US-10-339-217-104
  Sequence 104, Application US/10339217
Publication No. US20030198648A1
GENERAL INFORMATION:
APPLICANT: Buechter, Douglas
APPLICANT: Hou, Xiaohong
                                                                                         TTCGAGGAGACCACCCCCGGCCAGAAGCAGGAGGAGCAAGGACCGCGAGACCCTGACCAGC
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APPLICANT: Rice, William G.
APPLICANT: Yang, Wengang
TITLE OF INVENTION: Methods for Identifying Co-
TITLE OF INVENTION: Nucleocapsid 7 Protein to
FILE REFERENCE: 111021.143 (ACH-US1)
CURRENT APPLICATION NUMBER: US(10/339,217
CURRENT FILING DATE: 2003-01-09
PRIOR APPLICATION NUMBER: US 60/347,369
PRIOR FILING DATE: 2002-01-11
NUMBER OF SEQ ID NOS: 144
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 104
LENGTH: 491
TYPE: PRI
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; ORGANISM: HIV-1
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; Publication No. US20030198648A1
; GENERAL INFORMATION:
; APPLICANT: Buechter, Douglas
APPLICANT: Hou, Xiaohong
; APPLICANT: Marlor, Christopher W.
; APPLICANT: Rice, William G.
; APPLICANT: Yang, Wengang
; TITLE OF INVENTION: Nucleocapsid 7 Protein to
FILE REFERENCE: 111021.143(ACH-US1)
; CURRENT APPLICATION NUMBER: US/10/339,217
; CURRENT FILING DATE: 2003-01-09
; PRIOR APPLICATION NUMBER: US 60/347,369
; PRIOR FILING DATE: 2002-01-11
; NUMBER OF SEQ ID NOS: 144
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APPLICANT: Hou, Xiaohong
APPLICANT: Marlor, Christopher W.
APPLICANT: Rice, William G.
APPLICANT: Rice, William G.
APPLICANT: Yang, Wengang
TITLE OF INVENTION: Methods for Identifying Compounds Which Inhibit Binding of
TITLE OF INVENTION: Nucleocapsid 7 Protein to HIV-1 RNA
FILE REFERENCE: 111021.143(ACH-US1)
CURRENT APPLICATION NUMBER: US/10/339,217
CURRENT FILING DATE: 2003-01-09
PRIOR APPLICATION NUMBER: US 60/347,369
PRIOR APPLICATION NUMBER: US 60/347,369
PRIOR FILING DATE: 2002-01-11
NUMBER OF SEQ ID NOS: 144
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 108
LENGTH: 496
TYPE: PRT
ORGANISM: HIV-1
US-10-339-217-108
                       Alignment Scores: Pred. No.:
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APPLICANT: Buechter, Douglas
APPLICANT: Hou, Xiaohong
APPLICANT: Marlor, Christopl
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1 ATGGGCGCCGCGCCAGCATCCTGCGCGGCGGCAAGCTGGACGCCTGGGAGCGCATCCGC 60	Similarity: 95.94% cal Similarity: 91.08% atch: 85.91% 14	No.: 1.74e-117 Length: 2381.50 Matches:	; SOFTWARE: FastSEQ for Windows Version 4.0 ; SEQ ID NO 106 ; LENGTH: 487 ; TYPE: PRT ; ORGANISM: HIV-1 115-10-319-217-106	URRENT FILING DATE: 2003-01-09 RIOR APPLICATION NUMBER: US 60/347,369 RIOR FILING DATE: 2002-01-11 UMBER OF SEQ ID NOS: 144	TITLE OF INVENTION: Methods for Identifying Compounds Which Inhibit Binding of TITLE OF INVENTION: Nucleocapsid 7 Protein to HIV-1 RNA FILE REFERENCE: 111021.143 (ACH-US1) CURRENT APPLICATION NUMBER: US/10/319 217	PPLICANT: Hou, Xiaohong PPLICANT: Marlor, Christopher W. PPLICANT: Rice, William G. PPLICANT: Yang. Wengang		480 GluProLeuThrSerLeuLysSerLeuPheGlySerAspPı l 3-217-106	460 AlaGluSerPheArgPheGluGluIleThrProValProLysGlnGluProLysAspArg 479  1426 GAGACCCTGACCAGCCTGAAGAGCCTGTTCGGCAACGACCCCCTGAGCCAG 1476	66 GCCGAGAGCTTCCGCTTCGAGGAGACCACCCCCGGCCAGAAGCAGGAGAAGCAAGGACCGC 1	06 AGCCACAAGGGCCGCCCCGCAACTTCCTGCAGAGCCGCCCCGAGCCCAACCGCCCCCCC 1	1246 GGCCACCAGATGAAGGACTGCACCGAGCGCCAGGCCAACTTCCTGGGCAAGATCTGGCCC 1305	1186 CACATCGCCCGCAACTGCCGCGCCCCCCCGCAAGAAGGGCTGCTGGAAGTGCGGCAAGGAG 1245	380 AsnSerAsnPheLysGlySerArgArgIleValLysCysPheAsnCysGlyLysValGly 399	60 HistysAlaArgValLeuAlaGluAlaMetSerGlnThrAsnSerAsnIleMetMetGln 379	340 GIYPTOGIYALATNTLEUGIUGIUMETMETTNTALACY8GINGIYVAIGIYGIYPTOSET 359  1066 CACAAGGCCGGGTGCTGGCCGAGGCGATGAGCCAGCCAACACCAGCGTGATGATGCAG 1125	GGCCCGGCGCCAGCCTGGAGGAGATGATGACCGCCTGCCAGGGCGTGGGCGGCCCCAGC 1
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WS-10-339-217-107

Sequence 107, Application US/10339217;
Publication No. US20030198648A1

GENERAL INFORMATION:
APPLICANT: Buechter, Douglas
APPLICANT: Hou, Xiaohong
APPLICANT: Marlor, Christopher W.
APPLICANT: Yang, Wengang
TITLE OF INVENTION: Methods for Identifying Com
FILE REFERENCE: 111021.143 (ACH-US1)
CURRENT APPLICATION NUMBER: US/10/339,217
CURRENT APPLICATION NUMBER: US/0/347,369
PRIOR APPLICATION NUMBER: US 60/347,369
PRIOR FILING DATE: 2002-01-11
NUMBER OF SEQ ID NOS: 144
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 107
LENGTH: 497
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Best Local Similarity:
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                             AspCysThrGluArgGlnAlaAsnPheLeuGlyLysIleTrpProSerHisLysGlyArg
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Sequence 105, Application US/10339217

; Publication No. US20030198648A1

; GENERAL INFORMATION:

APPLICANT: Hou, Xiaohong

APPLICANT: Hou, Xiaohong

APPLICANT: Rice, William G.

APPLICANT: Yang, Wengang

TITLE OF INVENTION: Nucleocapsid 7 Protein to

FILE REFERENCE: 111021.143(ACH-US1)

CURRENT APPLICATION NUMBER: US/10/339,217

CURRENT FILING DATE: 2003-01-09

PRIOR APPLICATION NUMBER: US 60/347,369

PRIOR FILING DATE: 2002-01-11

NUMBER OF SEQ ID NOS: 144

SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 105

LENGTH: 508

TYPE: DET
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Best Local Similarity:
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; ORGANISM: HIV-1
US-10-339-217-105
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US-10-339-217-105
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Matches:
Conservative:
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                                          -----AGCCGCCCCGAGCCCACCGCCCCCCCCGAGAGCTTCCGCTTCGAGGAGSGAGSTPheArgAsnArgProGluProThrAlaProProAlaGluSerPheArgPheGluGlu
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       ThrThrProThrProLy8GInGluProLy8AspArgAspProLeuThrSerLeuLysSer
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Zur Megede, Jan

APPLICANT: Barnett, Susan W.

APPLICANT: Egnelbrecht, Susan

APPLICANT: Egnelbrecht, Susan

APPLICANT: van Rensburg, Estrelita Janse

TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C

TITLE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF

FILE REFERENCE: PP01631.102

CURRENT APPLICATION NUMBER: US/09/899,575

CURRENT FILING DATE: 2001-07-05

PRIOR APPLICATION NUMBER: 09/475,704

PRIOR FILING DATE: 1999-12-30

NUMBER OF SEQ ID NOS: 135

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 22

LENGTH: 502

TYPE: PRT

GRANISM: Human immunodeficiency virus

US-09-899-575-22
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GENERAL INFORMATION:

APPLICANT: Buechter, Douglas

APPLICANT: Hou, Xiaohong

APPLICANT: Marlor, Christopher W.

APPLICANT: Rice, William G.

APPLICANT: Yang, Wengang

TITLE OF INVENTION: Methods for Identifying Commendation

FILE REFERENCE: 111021.143(ACH-US1)

CURRENT APPLICATION NUMBER: US/10/339,217

CURRENT FILING DATE: 2003-01-09

PRIOR APPLICATION NUMBER: US 60/347,369

PRIOR FILING DATE: 2002-01-11

NUMBER OF SEQ ID NOS: 144

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 126

LENGTH: 494

TYPE: PRT

ORGANISM: HIV-1
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Search completed: March 11, 2005, 16:38:15 Job time: 200.728 secs

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Result
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-MODEL=frame+ n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US09475704/runat_10032005_140222_14851/app_query.fasta_1.3342
-Q=/cgn2_1/USPTO_spool_p/US09475704/runat_10032005_140222_14851/app_query.fasta_1.3342
-DB=Issued_patents_AA -QFMT=fastan -SUFFIX=n2p.rai -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits_START=1 -END=-1 -MATRIX=blosum62_-TRANS=human40.cdi
-LOOPEXT=0 -UNITS=bits_START=1 -END=-1 -MATRIX=blosum62_-TRANS=human40.cdi
-LIST=45_-DOCALIGN=200_-THR_SCORE=pct_-THR_MAX=100_-THR_MIN=0_-ALIGN=15
-MODE=LOCAL_-OUTFMT=pto_-NORM=ext_-HEAPSIZE=500_-MINLEN=0_-MAXLEN=2000000000
-USER=US09475704_@CGN_1_1_86_@runat_10032005_140222_14851_-NCPU=6_-ICPU=3
-NO_MMAP_-LARGEQUERY_-NEG_SCORES=0_-WAIT_-DSPBLOCK=100_-LONGLOG
-DEV_TIMEOUT=120_-WARN_TIMEOUT=30_-THREADS=1_-XGAPOP=10_-XGAPEXT=0.5_-FGAPOP=6
-FGAPEXT=7_-YGAPOP=10_-YGAPEXT=0.5_-DELOP=6_-DELEXT=7
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## ALIGNMENTS

Application US/09991258

APPLICANT:

Maughan, Maureen

```
APPLICANT: Johnston, Robert
APPLICANT: Davis, Nancy
APPLICANT: Swanstrom, Ronald
TITLE OF INVENTION: ALPHAVIRUS VECTORS AND V
TITLE OF INVENTION: VACCINES
FILE REFERENCE: 01113.0001U3
CURRENT APPLICATION NUMBER: US/09/991,258
CURRENT FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 09/902,537
PRIOR FILING DATE: 2001-07-09
PRIOR FILING DATE: 2000-07-07
INMBER OF SEQ ID NOS: 19
SOFTWARE: FASTSEQ for Windows Version 4.0
                     Pred. No.:
                                   Alignment Scores:
                                                                               US-09-991-258-5
                                                                                                                                                         SEQ ID NO 5
LENGTH: 492
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                               OTHER INFORMATION: Description of Artificial OTHER INFORMATION: synthetic construct
                                                                                                                                         FEATURE:
   2.97e-141
2435.00
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Length: Matches:
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Query Match:
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COUNTRY: CORDINER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/816,155B
FILING DATE: 12-MAR-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: KOWALSKI, THOMAS J.
REFERENCE/DOCKET NUMBER: 454310-29
REFERENCE/DOCKET NUMBER: 454310-29
TELECOMMUNICATION INFORMATION:
TELEPAX: 212-588-0800
TELEFAX: 212-588-0800
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
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US-08-816-155B-45
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APPLICANT: COX, WILLIAM I.
APPLICANT: GETTIG, RUSSELL R.
APPLICANT: MARTINEZ, HECTOR
APPLICANT: MARTINEZ, HECTOR
APPLICANT: PAOLETTI, ENZO
APPLICANT: PINCUS, STEVEN E.
APPLICANT: PINCUS, STEVEN E.
TITLE OF INVENTION: VECTORS HAVING ENHANCED EXITITLE OF INVENTION: METHODS OF MAKING AND USES
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSE: FROMMER LAWRENCE & HAUG LLP
STREET: 745 FIFTH AVENUE
CITY: NEW YORK
COUNTRY: USA
TID. 10151
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Sequence 45, Application US/09079587

Patent No. 6130066

GENERAL INFORMATION:
APPLICANT: TARTAGLIA, JAMES
APPLICANT: COX, WILLIAM I.
APPLICANT: GETTIG, RUSSELL R.
APPLICANT: GETTIG, RUSSELL R.
APPLICANT: PAOLETTI, ENZO
APPLICANT: PAOLETTI, ENZO
APPLICANT: PINCUS, STEVEN E.
TITLE OF INVENTION: VECTORS HAVING ENHANCED EXPRESSION, AND
TITLE OF INVENTION: METHODS OF MAKING AND USES THEREOF
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: FROMMER LAWRENCE & HAUG LLP
STREET: 745 FIFTH AVENUE
CITY: NEW YORK
COUNTRY: USA
ZIP: 10151
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEPHONE: 212-588-0800
TELEFAX: 212-588-0500
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 500 amino acids
TYPE: amino acid
STRANDEDNESS: n/a
TOPOLOGY: linear
MOLECULE TYPE: amino acid
US-09-079-587-45
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Best Local Similarity:
Query Match:
DB:
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FILING DATE: 12-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: KOWALSKI, THOMAS J.
REGISTRATION NUMBER: 32,147
REFERENCE/DOCKET NUMBER: 454310-2990
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US/09/079,587 FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
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RESULT 4
US-08-375-510-1
; Sequence 1, Application U; Patent No. 5576421
; GENERAL INFORMATION:
; APPLICANT: Saito, Ats:
; APPLICANT: Nakata, At
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 Saito, Atsushi
Sinagawa, Hidec
Nakata, Atsuo
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 500 amino acids
TYPE: amino acid
STRANDEDNESS: single
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APPLICATION NUMBER: US/07/985,949
FILING DATE: 04-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Svensson, Leonard R.
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 216-309P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 241-1300
TELEFAX: (703) 241-2848
                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE: ORGANISM: Human immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 22040-0747

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch
STREET: P.O. Box 747
CITY: Falls Church
STATE: Virginia
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE:
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                  LeuArgProGlyGlyLysLysGlnTyrLysLeuLysHisIleValTrpAlaSerArgGlu
 CTGGACAAGATCGAGGAGGAGCAGAACAAGTGCCAGCAGAAGATCCAGCAGGCCGAGGCC
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2249.00
92.22*
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Matches:
Conservative:
Mismatches:
Indels:
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                              US-09-475-704A-3 (1-1479) x US-08-487-657-1 (1-500)
                                                                                    Percent Similarity:
Best Local Similarity:
                                                                                                                             Pred. No.:
                                                                                                                                        Alignment Scores:
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                                                                                                                                                                                                                                            TELEFAX: (703) 241-2848
TELEX: 248345
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 500 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,657
FILING DATE: 07-JUN-1995
CLASSIFICATION ATA:
APPLICATION NUMBER: US/07/985,949
FILING DATE: 18-JAN-1995
APPLICATION NUMBER: US/07/985,949
FILING DATE: 04-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Svensson, Leonard R.
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 216-309P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 241-2848
TELEX: 248345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/08487657
Patent No. 5834267
GENERAL INFORMATION:
APPLICANT: Saito, Atsushi
APPLICANT: Sinagawa, Hideo
APPLICANT: Nakata, Atsuo
                                                                                                                                                                               HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE: ORGANISM: Human
                                                                                                                                                                                                                                 MOLECULE TYPE:
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APPLICANT: Nakata, Atsuo
TITLE OF INVENTION: HIV ANTIGEN
NUMBER OF SEQUENCES: 4
                                                                        Match:
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: P.O. Box 7.
CITY: Falls Church
STATE: Virginia
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Matches:
Conservative:
Mismatches:
Indels:
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APPLICANT: Heinrich-Pette-Institut
TITLE OF INVENTION: Retroviral hybrid vectors pseudotyped with LCMV
FILE REFERENCE: p50489
CURRENT APPLICATION NUMBER: US/09/309,572
CURRENT FILING DATE: 1999-05-11
EARLIER APPLICATION NUMBER: DE 198 56 463
EARLIER FILING DATE: 1998-11-26
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.0
EQ ID NO 16
LENGTH: 500
TYPE: PRT
ORGANISM: Human immunodeficiency virus type 1
FEATURE:
OTHER INFORMATION: gag polyprotein
US-09-309-572-16
                                                                                                                                                                                                                                                                        RESULT 6
US-09-309-572-16
US-09-309-572-16
; Sequence 16, Application US/09309572
; Patent No. 6440730
; GENERAL INFORMATION:
                                                                                                  Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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                            GGCCACCAGATGAAGGACTGCACCGAGCGCCAGGCCAACTTCCTGGGCAAGATCTGGCCC
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Matches:
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1 ACCGTGGCCACCCTGTACTGCGTGCACGAGAAGATCGAGGTCCGCGACACCAAGGAGGCC 3	QY 181 ATCCGCCAGCTGCACCCCGCCCTGCAGACCGGCAGCGAGGAGCTGAAGAGCCTGTTCAAC 240 :::           :::	Oy 121 CTGGAGAAGTTCGCCCTGAACCCCGGCCTGCTGGAGACCAGCGAGGGCTGCAAGCAGATC 180       :::      :::	Qy 61 CTGCGCCCGGCGCAAGAAGTGCTACATGATGAAGCACCTGGTGTGGGCCAGCCGCGAG 120 	Qy 1 ATGGGCGCCGCGCGCAGCATCCTGCGCGGCGGCAAGCTGGACGCCTGGGAGCGCATCCGC 60	n: 81.13% Indels: 4 Gaps: 704A-3 (1-1479) x US-09-718-096-16 (1-500)	Pred. No.: 6.92e-130 Length: 500 Score: 2249.00 Matches: 421 Percent Similarity: 92.22% Conservative: 41 Best Local Similarity: 84.03% Mismatches: 29	; OTHER INFORMATION: gag polyprotein US-09-718-096-16 Alignment Scores:	LENGTH: 500 TYPE: PRT ORGANISM: Human immunod FEATURE:	; PRIOR FILING DATE: 1999-05-11 ; NUMBER OF SEQ ID NOS: 26 ; SOFTWARE: Patentin Ver. 2.0 ; SEQ ID NO 16	PRIOR FILING DATE: 1998-11-26 PRIOR APPLICATION NUMBER: EP 99250415. PRIOR FILING DATE: 1999-11-25 PRIOR APPLICATION NUMBER: US 09/309,57	FILE REFERENCE: 35-195 CURRENT APPLICATION NUMBER: US/09/718,096 CURRENT FILING DATE: 2000-11-22 PRIOR APPLICATION NUMBER: DE 19856463.5	Patent No. 6589763 GENERAL INFORMATION: APPLICANT: Von Laer, Meike-Do TITLE OF INVENTION: RETROVIRA	RESULT 7 US-09-718-096-16 ; Sequence 16, Application US/09718096	Qy 1474 CAG 1476     Db 500 Gln 500	Qy 1420 GACCGCGAGACCCTGACCAGCCTGAAGAGCCTGTTCGGCAACGACCCCCTGAGC 1473    :::            :::            Db 480 AspLysGluLeuTyrProLeuAlaSerLeuArgSerLeuPheGlySerAspProSerSer 499	Qy 1366 GCCGAGAGCTTCCGCTTCGAGGAGACCACCCCCGGCCAGAAGCAGGAGAAGCAAG 1419	QY 1306 AGCCACAAGGGCCGCCCGGCAACTTCCTGCAGAGCCGCCCGAGCCCACCGCCCCCCC 1365	Qy 1246 GGCCACCAGATGAAGGACTGCACCGAGCGCCAGGCCAACTTCCTGGGCAAGATCTGGCCC 1305 
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121 CTGGAGAAGTTCGCCCTGAACCCCGGCCTGCTGGAGAGCCAGCGAGGGCGAGGGCAAGCAA	р—о С	1 ATGGGCGCCGCGCCAGCATCCTGCGCGCGGCAAGC	y Match:  80.99%  Indels:  Gaps:  9-475-704A-3 (1-1479) y HS-09-952-060-35 (1-1350)	Alignment Scores:  Pred. No.:  1.44e-129 Length:  Score:  2245.00 Matches:  Percent Similarity:  92.00% Conservative:  Heat Local Similarity:  81.80% Mignatches:  32	OTHER INFOR 9-952-060-3	4	PRIOR FILING DATE: 2000-09-15 NUMBER OF SEQ ID NOS: 38 SOFTWARE: FastSEQ for Windows Versi	PRIOR FILING DATE: 2001-09-07 PRIOR APPLICATION NUMBER: 60/279,0 PRIOR FILING DATE: 2001-03-27 PRIOR APPLICATION NUMBER: 60/233,1	CURRENT FILING DATE: 2001-09-14 PRIOR APPLICATION NUMBER: PCT/US01/28861 PRIOR FILING DATE: 2001-09-14 PRIOR APPLICATION NUMBER: 60/317,814	TITLE OF INVENTION: VACCINES EXPRESSING CODON TITLE OF INVENTION: MODIFICATIONS FILE REFERENCE: 20747Y  CURRENT APPLICATION NUMBER: US/09/952,060	; APPLICANT: Shiver, John W.; APPLICANT: Toner, Timothy J.; APPLICANT: Casimiro, Danilo R.; APPLICANT: Casimiro, Danilo R.; TITLE OF INVENTION: ENHANCED FIRST GENERATION ADENOVIRUS	APPLICAN APPLICAN APPLICAN APPLICAN	Sequence 35, Patent No. 67 GENERAL INFOR	5 ULT 8 09-952-0	74 CAG 1476	Qy 1420 GACCGCGAGACCCTGACCAGCCTGAAGAGCCTGTTCGGCAACGACCCCCTGAGC 1473    :::           :::	60 GluGluSerPheArgPheGlyGlu	Db 440 SerHisLysGlyArgProGlyAsnPheLeuGlnSerArgProGluProThrAlaProPro 459  Qy 1366 GCCGAGAGCTTCCGCTTCGAGGAGACCACCCCCGGCCAGAAGCAGGAGAGCAAG 1419
Q D QY	g Q	D Qy	₽ <i>Q</i>	D Q	Q dd	₽ <i>Q</i>	당 성	g Qy	g Q	d Q	d Q	g Q	B 84	gg Qy	Db :	Q D	Q	g Qy
1189 ATCGCCCGCAACTGCCGCCGCCCCCCCCAAGAAGGGCTGCTGGAAGTGCCGCCAAGAAGGAGGC 1248       :::	1129 AGCAACTTCAAGGGCCCCCGGCGATCGTCAAGTGCTTCAACTGCGGCAAGGAGGGCCAC 1188       :::	61	1015 GCCAGCCTGGAGGAGATGATGACCGCCTGCCAGGCGTGGGCGGCCGCCAGCCA	955 CTGCTGGTGCAGAACGCCAACCCCGACTGCAAGACCATCCTGCGCGCTCTCGGCCCCGGC 1014 	895 TTCAAGACCCTGCGCGCGAGCAGCAGCACCCCAGGAGGTGAAGAACTGGATGACCGACACC 954 :::                    :::::	835 AGCATCCTGGACATCAAGCAGGGCCCCAAGGAGCCCTTCCGCGACTACGTGGACCGCTTC 894 	775 ATCTACAAGCGGTGGATCATCCTGGGCCTGAACAAGATCGTGCGGATGTACAGCCCCGTG 834	15 41	μ <sub>0</sub>	595 CTGAAGGACACCATCAACGAGGAGGCCGCCGAGTGGGACCGCGTGCACCCCCGTGCACGCC 654	535 CCCCAGGACCTGAACACGATGTTGAACACCGTGGGCGGCCACCAGGCCGCCATGCAGATG 594	475 GAGAAGGCCTTCAGCCCCGAGGTGATCCCCCATGTTCACCGCCCTGAGCGAGGGCGCCCACC 534	415 CAGATGGTGCACCAGGCCATCAGCCCCCGCACCCTGAACGCCTGGGTGAAGGTGATCGAG 474	361GCCGACAAGGGCAAGGTGAGCCAGAACTACCCCATCGTGCAGAACCTGCAGGGC 414 ::: :::	:::	81 ThrValAlaThrLeuTyrCysValHisGlnLysIleAspValLysAspThrLysGluAla 100 301 CTGGACAAGATCGAGGAGGAGCAGAACAAGTGCCAGCAGAAGATCCAGCAGGCCGAGGCC 360	1 ACCGTGGCCACCCTGTACTGCGTGCACGAGAAGATCGAGGTCCGCGACACCAAGGI	181 ATCCGCCAGCTGCACCCCGCCCTGCAGACCGGCAGCGAGGAGCTGAAGAGCCTGTTCAAC 240  :::           :::

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APPLICANT: GALLO, Robert C.
APPLICANT: WONG-STAAL, Flossie
TITLE OF INVENTION: CLONING AND EXPRESSION OF NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: MOTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No.
                                                                                                                                                                                                                                 TELEFAX: (212) 751-6849 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/693,866
FILING DATE: 23-JAN-1985
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/659,339
                                                                                                                               MOLECULE TYPE: protein HYPOTHETICAL: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 10154-0053

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,210
FILING DATE: 05-JUN-1995
                                                                                                                                                                                                                                                      FILING DATE: 10-OCT-1984
ATTORNEY/AGENT INFORMATION:
NAME: Serunian, Leslie A.
REGISTRATION NUMBER: 35,353
REFERENCE/DOCKET NUMBER: 2026-4193US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                 NAME/KEY: Protein LOCATION: 1.512 OTHER INFORMATION:
                                                                                                                                                                               LENGTH: 512 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                    ORGANISM:
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CITY: New York
STATE: New York
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Sequence 2, Application US/09124900
; Patent No. 6268484
; GENERAL INFORMATION:
APPLICANT: KATINGER, Hermann
APPLICANT: BUCHACHER, Andrea
APPLICANT: BYCHACHER, Martin
APPLICANT: PURTSCHER, Martin
APPLICANT: PURTSCHER, Martin
APPLICANT: PREDL, Renate
APPLICANT: SCHMATZ, Christine
APPLICANT: KLIMA, Annelies
APPLICANT: MUSTER, Thomas
TITLE OF INVENTION: HIV-Vaccines
FILE REFERENCE: 1939-112P
CURRENT APPLICATION NUMBER: US/09/124,900
CURRENT FILING DATE: 1998-07-30
PRIOR APPLICATION NUMBER: PCT/EP95/01481
PRIOR FILING DATE: 1995-04-19
INUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 512
                           Alignment Scores: Pred. No.:
                                                    ; TYPE: PRT
; ORGANISM: Human
US-09-124-900-2
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US-09-124-900-2
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US-08-463-028-8
; Sequence 8, Application US/08463028
; Patent No. 6610476
; GENERAL INFORMATION:
ZIP: 10154-0053
ZIP: 10154-0053
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,028
FILING DATE: 05-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 06/693,866
FILING DATE: 23-JAN-1985
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/659,339
FILING DATE: 10-OCT-1984
ATTORNEY/AGENT INFORMATION:
NAME: Serunian, Leslie A.
REGISTRATION NUMBER: 35,353
REFERENCE/DOCKET NUMBER: 2026-4193US3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: CHANG, Nancy T.
APPLICANT: GALLO, Robert C.
APPLICANT: WONG-STAAL, Flossie
TITLE OF INVENTION: CLONING AND
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan &
STREET: 345 Park Ave.
                                                                                                                                                                                                                                                                                      CITY: New York
STATE: New York
COUNTRY: USA
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TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
ELNGTH: 512 amino acids
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ORIGINAL SOURCE
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TYPE: amino acid
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RESULT 11

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Sequence 33, Application US/0995; Patent No. 6733993; GENERAL INFORMATION:
APPLICANT: Emini, Emilio A. APPLICANT: Youil, Rima APPLICANT: Bett, Andrew J. APPLICANT: Chen, Ling APPLICANT: Kaslow, David C. APPLICANT: Shiver, John W. APPLICANT: Toner, Timothy J. APPLICANT: Casimiro, Danilo R. TITLE OF INVENTION: ENHANCED FI
                                                                                                                 RESULT 12
US-09-952-060-33
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FILE REFERENCE: 20747Y

CURRENT APPLICATION NUMBER: US/09/952,060

CURRENT FILING DATE: 2001-09-14

PRIOR APPLICATION NUMBER: 60/317,814

PRIOR APPLICATION NUMBER: 60/317,814

PRIOR FILING DATE: 2001-09-07

PRIOR FILING DATE: 2001-09-07

PRIOR APPLICATION NUMBER: 60/279,056

PRIOR FILING DATE: 2001-03-27

PRIOR APPLICATION NUMBER: 60/233,180

PRIOR APPLICATION NUMBER: 60/233,180

PRIOR FILING DATE: 2000-09-15

NUMBER OF SEQ ID NOS: 38

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 33

LENGTH: 493

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OTHER INFORMATION: tPA-gag
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                                                                                                  Sequence 11, Application US/08127499A
Patent No. 5510264

GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED
TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                          STATE: D.C. COUNTRY: US
                                                       STREET: 3000 K St
CITY: Washington
                                                                        ADDRESSEE: Foley & Lardner STREET: 3000 K Street, N.W.,
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/127,499A

FILING DATE: 28-SEP-1993

ATTORNEY/AGENT INFORMATION:

NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 51916/102/INBI

TELECOMMUNICATION INFORMATION:
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TELEX: 904136
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
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TELEFAX: (202)672-5399
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                                                                                    GAGGAGAAGGCCTTCAGCCCCGAGGTGATCCCCCATGTTCACCGCCCTGAGCGAGGGCGCCC
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Matches:
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COUNTRY: USA

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Sequence 11, Application US/08482847

Patent No. 5556757

GENERAL INFORMATION:
APPLICANT: VAN ALSTYNE, Diane
APPLICANT: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AG
TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                         CACATCGCCCGCAACTGCCGCGCCCCCCCGCAAGAAGGGCTGCTGGAAGTGCGGCAAGGAG
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TELEX: 904136
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
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APPLICATION NUMBER: US 08/127
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 5191
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5399
TELEPAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                          GGCCAGATGGTGCACCAGGCCATCAGCCCCCGCACCCTGAACGCCTGGGTGAAGGTGATC
                                                                                    GCCGACAAGGGC-----AAGGTGAGCCAGAACTACCCCATCGTGCAGAACCTGCAG
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RESULT 14 US-08-482-847-11

ADDRESSEE: Foley & Lardner STREET: 3000 K Street, N.W., CITY: Washington STATE: D.C.

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RESULT 15
US-08-392-794A-2
     Sequence 2, Application US/08392794A
Patent No. 6025141
GENERAL INFORMATION:
APPLICANT: HU, Yu-Wen
TITLE OF INVENTION: IMMUNOFLUORESCENCE ASSAY FOR
TITLE OF INVENTION: ANTIBODIES USING RECOMBINANT
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/392,794A
FILING DATE: 09-DEC-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 202-628-51
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO:
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FILING DATE: 10-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: NEIMARK, SHERIDAN
REGISTRATION NUMBER: 20,52
REFERENCE/DOCKET NUMBER: H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 437 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: BROWDY AND NEIMARK STREET: 419 Seventh Street, N.W CITY: Washington STATE: D.C. COUNTRY: USA ZIP: 20004
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MEDIUM TYPE: Floppy of COMPUTER: IBM PC com
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Search completed: March 11, 2005, Job time: 73.8258 secs

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OLASIN ANKATE BENEATH INSERTION

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Result
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-MODEL=frame+ n2p.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US09475704/runat_10032005_140220_14808/app_query.fasta_1.3342
-DB=A Geneseq_16Dec04 -QFMT=fastan -SUFFIX=n2p.rag -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -THR_MS=human40.cdi
-LOST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=20000000
-USER=US09475704_@CGN_11_472_@runat_10032005_140220_14808 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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1: geneseqp1980s:*
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Aae37600 HIV-1 sub
Adp02848 Wild type
Adp02847 Wild type
Adn36396 Human pro
Aae18303 Human imm
Aam48948 HIV-1 sub
Adc72880 HIV-1 gag
Adn36406 Human pro
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AAP80885
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86196
96944
ADC72875
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ADC72913
AAB69278
72874
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## ALIGNMENTS

RESULT 1
AAY96943
ID AAY9
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AC AAY9
AC AAY9
XX
OE HIV
XX
KW Gag;
KW DNA
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OS Synt
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OS Synt
XX
PD 06-J
XX
PF 30-D
XX
PR 01-S
XX
PR 01-S
XX
PR WPI;
DR WPI;
DR WPI;
DR POly
PT Poly WPI; 2000-452401/39. N-PSDB; AAA51609. Barnett S, 30-DEC-1999; Human immunodeficiency virus; type C strain AF110965. Synthetic. Gag; expression cassette; antigenic; type C; HIV; Env; synthetic; DNA immunization; packaging cell line; antigen presentation. HIV synthetic Gag polypeptide. 31-OCT-2000 (first entry) AAY96943 standard; protein; 31-DEC-1998; 01-SEP-1999; WO200039304-A2 AAY96943; 06-JUL-2000. (CHIR ) CHIRON CORP Zur Megede 98US-0114495P. 99US-0152195P. 99WO-US031273 J; 492 AA

Polynucleotide encoding antigenic type C HIV Gag polypeptide or polypeptide and the polypeptide useful for immunizing a mammal e

r a HIV Env especially

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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to molecules comprising HIV-1 subtype isolate regulatory/accessory genes (tat, nef and rev genes) and modifications and derivatives thereof. The invention also provides proteins encoded by such genes. Sequences of the invention are useful for manufacturing vaccines for treating or preventing human immunodeficiency virus (HIV) infections.
                                                                                                                                                                                                                                                                                                                                                                               For treating or preventing human immunodeficiency virus (HIV) infect
They are also useful in gene therapy. The present sequence is HIV-1
subtype C isolate Du422 Gag protein. (Updated on 23-OCT-2003 to
standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genes, useful
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for the treatment or prophylaxis of HIV
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                                                                                                                                                                                                 le invention relates to a nucleic acid vector comprising at least one IV sequence operably linked to a promoter and encoding a protein that les not assemble into viral particles. The nucleic acid vector is useful immunizing a subject against HIV infection. This sequence corresponds a peptide used in the invention.
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The invention relates to a composition comprising isolated nucleic acids encoding env, gag or pol gene product of human immunodeficiency virus or immunogenic fragment of the gene products. The gag gene product is modified to inhibit formation of virus-like particles containing gag gene product and their release from cells, and the pol gene product is modified to inhibit reverse transcriptase activity. The invention also relates to a method for producing an alpha-virus replicon particle used in vaccines. The composition is useful for inducing an immune response to human immunodeficiency virus (HIV) or for treating or preventing HIV infection in a subject. The alpha-virus replicon particle is useful in a
                                                                                                                                    Composition useful for treating or preventing HIV inf
two or more isolated nucleic acids encoding env, gag
of HIV or immunogenic fragment of the gene products.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vaccine. The composition is useful for administering a protein or peptide to a subject. A composition comprising heparin affinity-purified alphavirus replicon particle is useful as a clinical trial material and as a commercial product. The present sequence is HIV-1 Clade C gag protein. (Updated on 29-AUG-2003 to standardise OS field)
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GCCGACAAGGGCAAGGTGAGCCAGAACTACCCCCATCGTGCAGAACCTGCAGGGCCAGATG
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-GlyLysValSerGlnAsnTyrProIleValGlnAsnLeuGlnGlyGlnMet

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10-JUL-2000;
15-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to a process for the selection of human immunodeficiency virus (HIV) subtype isolates for use in the development of a prophylactic and/or therapeutic pharmaceutical composition. The process involves selecting isolated virus or viruses with a high sequence identity to a consensus sequence and a phenotype which is associated with transmission for the particular HIV subtype. The composition can be used in the production of vaccines against HIV. The present sequence is the HIV-1 subtype C isolate Du422 gag protein. (Updated on 29-AUG-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Selecting HIV-1 subtype C isolates, which are useful in developing vaccines against HIV infection, comprises isolating viruses with high sequence identity to a consensus sequence whose phenotype is associate with the HIV subtype.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Method of determining whether a compound inhibits formation of complex between HIV nucleocapsid protein 7 polypeptide and HIV psi-site oligonucleotide by comparing amount of complex formed in presence/absence
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                 LeuGluArgPheSerLeuAsnProGlyLeuLeuGluThrSerGluGlyCysLysGlnIle
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                                    AsnCysArgAlaProArgLysLysGlyCysTrpLysCysGlyLysGluGlyHisGlnMet
                                                          AACTGCCGCGCCCCCCCCAAGAAGGGCTGCTGGAAGTGCGGCAAGGAGGGCCCACCAGATG
                                                                                  AAGGGCCCCCGGCGATCGTCAAGTGCTTCAACTGCGGCAAGGAGGGCCACATCGCCCGC
                                                                                                                                                CTGGCCGAGGCGATGAGCCAGGCC---AACACCAGCGTGATGATGCAGAAGAGCAACTTC
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                                                                                                                                                                                                                                                                                                         The invention relates to a nucleic acid vector comprising at least one HIV sequence operably linked to a promoter and encoding a protein that does not assemble into viral particles. The nucleic acid vector is useful in immunizing a subject against HIV infection. This sequence corresponds to a peptide used in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid vector comprising at least one HIV sequence operably linked to a promoter and encoding a protein that does not assemble into viral particles, useful in immunizing a subject against HIV infection.
                                                                                                                                                                                                                                                       Sequence 1457
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N-PSDB; ADN36405.
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           GGCCCCCGGCGCATCGTCAAGTGCTTCAACTGCGGCAAGGAGGGCCCACATCGCCCGCAAC
                                                        CTGGCCGAGGCGATGAGCCAGGCCAACACCAGCGTGATGATGCAGAAGAGCAACTTCAAG
                                                                           ThrLeuArgAlaGluGlnAlaThrGlnAspValLysAsnTrpMetThrAspThrLeuLeu
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                                           LeuLysSerLeuPheGlySerAspProLeuSerGln
                                                                                                      TTCGAGGAGACCACCCCCGGCCAGAAGCAGGAGGCAAGGACCGCGAGACCCCTGACCAGC
                                                                                                                                                CCCGGCAACTTCCTGCAGAGCCGCCCCGAGGCCCAGCCGCCCCCCCGCGAGAGCCTTCCGC
standard;
                                                                   CTGAAGAGCCTGTTCGGCAACGACCCCCTGAGCCAG 1476
                                                                                       PheGluGluThrThrProAlaProLysGlnGluProLysAspArgGluProLeuThrSer
                                                                                                                                                                                 AspCysThrGluArgGlnAlaAsnPheLeuGlyLysIleTrpProProHisLysGlyArg
protein;
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ADC72879;

18-DEC-2003

(first entry)

HIV-1 gag protein containing an NCp sequence, SEQ IJ ö

complex; HIV nucleocapsid protein 7; NCp7; HIV-psi-site; anti-HIV;

Human immunodeficiency virus

WO2003060098-A2

10-JAN-2003; 2003WO-US000801

11-JAN-2002; 2002US-0347369P

(ACHI-) ACHILLION PHARM INC

Ö × Marlor £ Rice ຂັ ດີ Yang

Ξ

Method of determining whether a compound inhibits formation of complex between HIV nucleocapsid protein 7 polypeptide and HIV psi-site oligonucleotide by comparing amount of complex formed in presence/abserof compound. presence/absence

Claim SEQ ID NO 105pp; English.

The invention relates to a novel method of determining whether a compound inhibits formation of a complex between HIV nucleocapsid protein 7 (NCp7) polypeptide and an HIV-psi-site oligonucleotide. The method involves adding the HIV-psi-site oligo to a mixture of the NCp7 polypeptide and the novel compound and comparing amount of complex formed, with that formed in the absence of the compound, where a decrease in the amount of complex formed in presence of the compound indicates that the compound inhibits complex formation. The method of the invention involves anti-HIV activity. The compounds identified are useful for treating a subject infected with human immunodeficiency virus (HIV) by administering the compound to the subject. This sequence represents an HIV-1 gag protein which contains an NCp sequence of the invention.

Sequence 492 B ð

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AC AAB69
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DT 20-AF
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HIV-1
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HIV-1
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                            Novel genomic nucleic acids type 1 useful for detecting nucleotide sequence.
                                                            WPI; 2000-365651/31.
                                                                                                        02-NOV-1998;
                                                                                                                                       11-MAY-2000.
                                                                                                                                                      WO200026416-A1
                                                                                                                                                                   Human immunodeficiency virus
                                                                                                                                                                                  HIV-1; human immunodeficiency virus; vif; vpr; tat; rev; nef; vaccine.
                                                                                                                                                                                                        HIV-1 non-subtype B clone 96ZM651-8
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20-APR-2001
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                                   of non-subtype B human immunodeficiency virus and treating AIDS comprises a specific
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Claim 41; Fig 14; 131pp; English

present

in invention provides the protein and coding sequences for

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ATCTACAAGCGGTGGATCATCCTGGGCCTGAACAAGATCGTGCGGATGTACAGCCCCGTG
                                                                 GGCCCCATCGCCCCGGCCAGATGCGCGAGCCCCGCGGCAGCGACATCGCCGGCACCACC
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91.92%
87.16%
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RESULT 12
ADC72910
ADC72910
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                                                                       10-JAN-2003;
                                                                                                                                              immunodeficiency virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Method of determining whether a compound inhibits formation of complex between HIV nucleocapsid protein 7 polypeptide and HIV psi-site oligonucleotide by comparing amount of complex formed in presence/absence of compound.
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complex; HIV nucleocapsid protein 7; NCp7; HIV-psi-site; anti-HIV;

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entry)

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                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a novel method of determining whether a compound inhibits formation of a complex between HIV nucleocapsid protein 7 (NCp7) polypeptide and an HIV-psi-site oligonucleotide. The method involves adding the HIV-psi-site oligo to a mixture of the NCp7 polypeptide and the novel compound and comparing amount of complex formed, with that formed in the absence of the compound, where a decrease in the amount of complex formed in presence of the compound indicates that the compound inhibits complex formation. The method of the invention involves anti-HIV activity. The compounds identified are useful for treating a subject infected with human immunodeficiency virus (HIV) by administering the compound to the subject. This sequence represents an HIV-1 gag protein which contains an NCp sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Method of determining whether a compound inhibits formation of complex between HIV nucleocapsid protein 7 polypeptide and HIV psi-site oligonucleotide by comparing amount of complex formed in presence/absence of compound.
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type 1 useful for detecting and
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                   LeuGluGluMetValThrAlaCysGlnGlyValGlyGlyProSerHisLysAlaArgVal
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                                                                                                       The invention relates to a novel method of determining whether a compound inhibits formation of a complex between HIV nucleocapsid protein 7 (NCp7) polypeptide and an HIV-psi-site oligonucleotide. The method involves adding the HIV-psi-site oligo to a mixture of the NCp7 polypeptide and the novel compound and comparing amount of complex formed, with that formed in the absence of the compound, where a decrease in the amount of complex formed in presence of the compound indicates that the compound inhibits complex formation. The method of the invention involves anti-HIV activity. The compounds identified are useful for treating a subject infected with human immunodeficiency virus (HIV) by administering the compound to the subject. This sequence represents an HIV-1 gag protein which contains an NCp sequence of the invention.
                                                                                                                                                                                                                                                     Claim
                                                                                                                                                                                                                                                                           between HIV nucl oligonucleotide of compound.
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-DB=PIR 79 -QFMT=fastan -SUFFIX=n2p.rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
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-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09475704 @CGN 1 1 160 @runat 10032005 140222 14839 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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      Pred. No.
   Score

    No. is the number of results predicted by chance to have a
re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.

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ALIGNMENTS

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ĭ	ag protein -	gag protein - huma	ŝ		gag protein - feli	olyprotein	protein -		pro	pro	pro	m	pro		gag protein - huma	GAG protein - huma	gag polyprotein -	gag protein - simi		polyprote	polyprote		olyprote	polyprote						

## gag polyprotein - human immunodeficiency virus type 1 C;Species: human immunodeficiency virus type 1, HIV-1 C;Date: 15-Jul-1995 #sequence\_revision 01-Sep-1995 #tc;Accession: S54377 R;Theodore, T.; Buckler-White, A.J. submitted to the EMBL Data Library, July 1989 A;Reference number: S54377 A;Accession: S54377 RESULT 1 S54377 C; Keywords: polyprotein A;Cross-references: UNIPROT:P12495; EMBL:M22639; NID:g329377; PIDN:AAA45365.1; PID:g329:C;Superfamily: AIDS-related virus gag polyprotein US-09-475-704A-3 (1-1479) x S54377 (1-501) Query Match: Percent Similarity: Best Local Similarity: Score: A;Molecule type: genomic RNA A;Residues: 1-501 <THE> A; Status: preliminary Pred. No.: Alignment Scores: 121 41 21 61 CTGGAGAAGTTCGCCCTGAACCCCGGCCTGCTGGAGACCAGCGAGGGCTGCAAGCAGATC 180 LeuGluArgPheAlaLeuAsnProGlyLeuLeuGluThrSerAspGlyCysLysGinIle CTGCGCCCCGGCGCAAGAAGTGCTACATGATGAAGCACCTGGTGTGGGCCAGCCGCGAG 1.03e-109 2300.50 93.21% 86.63% 82.99% Conservative: Mismatches: Indels: Gaps: Length: Matches: #text\_change 120 40 60 20 60

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A;Gene: gag
A;Gene: gag
C;Superfamily: AIDS-related virus gag polyprotein
C;Keywords: AIDS; core protein; immunodeficiency; polyprotein
F;1-129/Product: core protein p17 #status predicted <C17>
F;130-389/Product: core protein p24 #status predicted <C24>
F;390-497/Product: core protein p15 #status predicted <C15>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: DNA
A;Residues: 1-497 <SPI>
A;Cross-references: UNIPROT:P18800;
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gag polyprotein - human immunodeficiency virus type 1 (isolate NDK)
N;Alternate names: core polyprotein
N;Contains: core protein p15; core protein p17; core protein p24
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: JQ0065
R;Spire, B; Sire, J; Zachar, V.; Rey, F.; Barre-Sinoussi, F.; Galibert, F.; Hampe,
Gene 81, 275-284, 1989
A;Title: Nucleotide sequence of HIV1-NDK: a highly cytopathic strain of the human imma, Reference number: JQ0065; MUID:90034200; PMID:2806917
A;Accession: JQ0065
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gag polyprotein - human immunodeficiency virus type 1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 09-.
C;Accession: T01667
R;Alizon, M.; Wain-Hobson, S.; Gluckman, J.C.; Sonigo, P.
Cell 46, 63-74, 1986
A;Title: Genetic variability of the AIDS virus: Nucleotide sequence A;Reference number: Z14389; MUID:86245056; PMID:2424612
A;Accession: T01667
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-505 <ALI>A;Cross-references: UNIPROT:P04594; EMBL:K03456; NID:g60228; PIDN:C;Superfamily: AIDS-related virus gag polyprotein
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RESULT 4
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gag polyprotein - human immunodeficiency virus type 1 (isolate LAV-1a)
N;Alternate names: assemblin; core polyprotein; gag precursor
N;Contains: capsid antigen core protein p24CA; core protein p1; core p
C;Species: human immunodeficiency virus type 1, HIV-1
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C;Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change
C;Accession: A03946
R;Wain-Hobson, S.; Sonigo, P.; Danos, O.; Cole, S.; Alizon, M.
Cell 40, 9-17, 1985
A;Title: Nucleotide sequence of the AIDS virus, LAV.
A;Reference number: A90866; MUID:85099333; PMID:2981635
A;Accession: A03946
A;Molecule type: DNA
A;Residues: 1-500 <WAI>
C;Genetics:
A;Gene: gag
C;Superfamily: AIDS-related virus gag polyprotein
C;Keywords: AIDS; blocked amino end; core protein; immunodefic:
F;2-500/Product: matrix antigen core protein p17MA #status pred;
F;2-32/Product: capsid antigen core protein p17MA #status pred;
F;2-132/Product: capsid antigen core protein p24CA #status pred;
F;378-432/Product: core protein p3 #status predicted <CP2>
F;378-432/Product: core protein p6 #status predicted <CP1>
F;243-448/Product: core protein p6 #status predicted <CP1>
F;249-500/Product: core protein p6 #status predicted <CP1>
F;27Modified site: myristylated amino end (Gly) (In mature form F;392,395,400,405/Binding site: zinc (Cys, Cys, His, Cys) #status p32,395,400,405/Binding site: zinc (Cys, Cys, His, Cys) #status p32,395,400,405/Binding site: zinc (Cys, Cys, His, Cys) #status p34 #status p34 #status p32,395,400,405/Binding site: zinc (Cys, Cys, His, Cys) #status p34 #status p34 #status p32,395,400,405/Binding site: zinc (Cys, Cys, His, Cys) #status p34 #status p34 #status p32,395,400,405/Binding site: zinc (Cys, Cys, His, Cys) #status p32,395,400,405/Binding site: zinc (Cys, Cys, His, Cys) #status p34 #status
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A;Title: Molecular cloning and primary nucleotide sequence analysis of a distinct human A;Reference number: A94136; MUID:87041461; PMID:3490666
A;Accession: A25523
A;Molecule type: DNA
A;Residues: 1-500 <DES>
A;Cross-references: UNIPROT:P05887; GB:M13136; NID:g326459; PIDN:AAA44306.1; PID:g32646.
C;Genetics:
A;Gene: gag
C;Superfamily: AIDS-related virus gag polyprotein
C;Keywords: core protein; polyprotein
F;1-132/Product: core protein p17 #status predicted <P17>
F;133-391/Product: core protein p24 #status predicted <P17>
F;392-500/Product: core protein p15 #status predicted <P15>
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N;Contains: core protein p15; core protein p17; core protein p24
C;Species: human immunodeficiency virus type 1, HIV-1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
C;Accession: A25523
R;Desai, S.M.; Kalyanaraman, V.S.; Casey, J.M.; Srinivasan, A.; Andersen, PProc. Natl. Acad. Sci. U.S.A. 83, 8380-8384, 1986
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gag polyprotein - human immunodeficiency virus type 1 (isolate A. N;Alternate names: core polyprotein N;Contains: core protein p15; core protein p17; core protein p24 C;Species: human immunodeficiency virus type 1, HIV-1 A;Note: host Homo sapiens (man) C;Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change C;Accession: A03947 R;Sanchez-Pescador, R.; Power, M.D.; Barr, P.J.; Steimer, K.S.; Science 227, 484-492, 1985
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            HisAlaGlyProIleAlaProGlyGlnMetArgGluProArgGlySerAspIleAlaGly
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A;Title: Nucleotide sequence and expression of an AIDS-associated retrovirus A;Reference number: A04003; MUID:85090453; PMID:2578227
A;Accession: A03947
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-502 <SAN>
A;Cross-references: UNIPROT:P03349; GB:K02007; NID:g328658; PIDN:AAB59875.1; A;Cross-references: UNIPROT:P03349; GB:K02007; NID:g328658; PIDN:AAB59875.1; A;Cross-references: UNIPROT:P03349; GB:K02007; NID:g328658; PIDN:AAB59875.1; A;Cross-references: UNIPROT:P03349; GB:K02007; NID:g328658; PIDN:AAB59875.1; A;Cross-references: UNIPROT:P03349; GB:K02007; NID:g328658; PIDN:AAB59875.1; A;Cross-references: UNIPROT:P03349; GB:K02007; NID:g328658; PIDN:AAB59875.1; A;Cross-references: UNIPROT:P03349; GB:K02007; NID:g328658; PIDN:AAB59875.1; A;Cross-references: UNIPROT:P03349; GB:K02007; NID:g328658; PIDN:AAB59875.1; A;Cross-references: UNIPROT:P03349; GB:K02007; NID:g328658; PIDN:AAB59875.1; A;Cross-references: UNIPROT:P03349; GB:K02007; NID:g328658; PIDN:AAB59875.1; A;Cross-references: UNIPROT:P03349; GB:K02007; NID:g328658; PIDN:AAB59875.1; A;Cross-references: UNIPROT:P03349; GB:K02007; NID:g328658; PIDN:AAB59875.1; A;Cross-references: UNIPROT:P03349; GB:K02007; NID:g328658; PIDN:AAB59875.1; A;Cross-references: UNIPROT:P03349; GB:K02007; NID:g328658; PIDN:AAB59875.1; A;Cross-references: UNIPROT:P03349; GB:K02007; NID:g328658; PIDN:AAB59875.1; A;Cross-references: UNIPROT:P03349; GB:K02007; NID:g328658; PIDN:AAB59875.1; A;Cross-references: UNIPROT:P03349; GB:K02007; NID:g328658; PIDN:AAB59875.1; A;Cross-references: UNIPROT:P03349; GB:K02007; NID:g328658; PIDN:AAB59875.1; A;Cross-references: UNIPROT:P03349; GB:K02007; NID:g328658; PIDN:AAB59875.1; A;Cross-references: UNIPROT:P03349; GB:K02007; NID:g328658; PIDN:AAB59875.1; A;Cross-references:UNIPROT:P03349; GB:K02007; NID:g328658; PIDN:AAB59875.1; A;Cross-references:UNIPROT:P03349; GB:K02007; NID:g328658; PIDN:AAB59875.1; A;Cross-references:UNIPROT:P03349; GB:K02007; NID:g328658; PIDN:AAB59875.1; A;Cross-references:UNIPROT:P03349; GB:K02007; NID:g328658; 
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                                                                                                                                                                                                                                                                                                                                                                                    CACGCCGGCCCATCGCCCCCGGCCAGATGCGCGAGCCCCCGCGGCAGCGACATCGCCGGC
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C;Accession: A03945
R;Ratner, L.; Haseltine, W.; Patarca, R.; Livak nberger, J.A.; Papas, T.S.; Ghrayeb, J.; Chang, Nature 313, 277-284, 1985
A;Title: Complete nucleotide sequence of the AII A;Reference number: A93353; MUID:85111123; PMID A;Accession: A03945
A;Molecule type: DNA
A;Residues: 1-512 <RAT>
                                                                                                                                RESULT
FOVWH3
                                                                           gag polyprotein - human immunodeficiency virus type 1 (isolate HTLV-III, BH: N;Alternate names: core polyprotein N;Contains: core protein p15; core protein p17; core protein p24 C;Species: human immunodeficiency virus type 1, HIV-1 A;Note: host Homo sapiens (man) C;Date: 17-May-1985 #text_change 09-Jul-2004 C;Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 09-Jul-2004
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Chang, N.T.;
                            ne AIDS virus,
PMID:2578615
                                                            K.J.;
                                                     Gallo,
                                                    Starcich, B.;
Ballo, R.C.; Wo
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82.65%
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651 199 591 179

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A;Cross-references: UNIPROT:P03347; GB:M15654; GB:K02008; GB:K C;Comment: Cleavage sites that yield the mature core proteins C;Genetics:
A;Gene: gag
C;Superfamily: AIDS-related virus gag polyprotein C;Keywords: AIDS; core protein; immunodeficiency; polyprotein F;1-132/Product: core protein p17 #status predicted <P17>F;133-391/Product: core protein p24 #status predicted <P24>F;392-512/Product: core protein p15 #status predicted <P15>
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Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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RESULT 8
T09436
T09436
gag polyprotein - human immunodeficiency virus type 1 (strain JRFL)
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T09436
R;Pang, S.; Vinters, H.V.; Akashi, T.; O'Brien, W.A.; Chen, I.S.; Koyanagi, submitted to the EMBL Data Library, July 1996
A;Reference number: Z16673
A;Accession: T09436
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Pred. No.:
Score:
                                                           A; Cross-references: C; Genetics:
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                                                                 LeuAspIleArgGlnGlyProLysGluProPheArgAspTyrValAspArgPheTyrLys
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720 220 660 200 540 160 300

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Alignment Scores:  Pred. No.:  231.00  Score:  Percent Similarity:  91.82%  Conservative:  40  Percent Similarity:  83.83%  Query Match:  1  1  Conservative:  40  Best Local Similarity:  80.48%  Indels:  10  US-09-475-704A-3 (1-1479) x A44001 (1-500)  Qy  1 ATGGGCGCCGCGCCAGCATCCTGCGGCGAAGCTGGAAGCTGGAAGCCTGGGAGCGCATCCGC 60	O01 polyprotein - human immunodeficiency virus type 1 (strain YU ternate names: core polyprotein ontains: core protein p15; core protein p17; core protein p24 pecies: human immunodeficiency virus type 1, HIV-1 ote: host Homo sapiens (man) ote: host Homo sapiens (man) ate: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change ccession: A44001 i, Y.; Hui, H.; Burgess, C.J.; Price, R.W.; Sharp, P.M.; Hahn virol. 66, 6587-6600, 1992 itle: Complete nucleotide sequence, genome organization, and eference number: A44001; MUID:93021387; PMID:1404605 ccession: A44001 ccession: A44001 olecule type: DNA esidues: 1-500 <liy> ross-references: UNIPROT:P35962; GB:M93258 enetics: ene: gag uperfamily: AIDS-related virus gag polyprotein ene: gag uperfamily: AIDS; core protein; immunodeficiency; polyprotein -132/Product: core protein p17 #status predicted <p17> 33-391/Product: core protein p15 #status predicted <p24> 92-500/Product: core protein p15 #status predicted <p24> 92-500/Product: core protein p15 #status predicted <p15></p15></p24></p24></p17></liy>	Oy 1021 CTGGAAGAATGATGACCGCCTGCCAGGGCGTTGGGCGCCCAGCCACAAGGCCCGCGTTG 1080
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952 ACCCTGCTGGTGCAGAACGCCAACCCCGACTGCAAGACCATCCTGCGCCCCCCCC	### InterprogramspleumsnThrMetLeumsnThrValGlyGlyHisGlnmalamataMetGln ### ATGCTGAAGGACACCATCAACGAGGAGGAGGCCGCCGAGTGGGACCGCGTGCACCCCGTGCACCCGTGCACCCATCAACGAGGAGGAGGCCGCCGAGTGGGACCGCGTGCACCCCGTGCACCCCGTGCACCCCGTGCACCCCGTGCACCCCGTGCACCCCGTGCACCCCGTGCACCCCGTGCACCCCGGCGCACCCCCGTGCACCCCCGTGCACCCCCCATCGCCCCCCGCGCCAGATGCGCCGCGCAGCCCCCCCC	

	Qy 181 ATCCGCCAGCCTGCACCCCGCCCTGCAGACCGGCAGCGAGAGAGCCTGAAGAGCCTGTTCAAC 240 :::	121 CTGGAGAAGTTCGCCCTGAACCCCGGCCTGCTGGAGACCAGCGAGGGCTGCAAGCAGATC 1	61 CTGCGCCCCGGCGAAGAAGTGCTACATGATGAAGCACCTGGTGTGGGCCAGCCGAG 1	1 ATGGGCGCCGCGCCAGCATCCT                 :::	ry Match: 80.38% Indels: 2 Gaps:	Scores: : imilarity:	A; ReBidues: 1-300 (CAK) A; Cross-references: UNIPROT:Q78240; EMBL:Z11530; NID:g60192; PIDN:CAA77621.1; PID:g60193 C; Superfamily: AIDS-related virus gag polyprotein	A; Accession: S33979 A; Status: preliminary A; Molecule type: mRNA	19-mar-1991 vember 1991		Db 500 Gln 500	1420 GACCGCG	460 GluGluSerValArgPheGlyGluGluThrThrThrProSerGlnLysGlnGluProIle 4	440 SerHisLysGlyArgProGlyAsnPheLeuGlnSerArgProGluProThrAlaProSer 459	1246 GGCCACCAGALGMAGGACIGCACCAGGCCAGGCCAGCCAGCCAGCCAGGCAGGCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCCAGGCA	:::	3lyAsnPheArgAsnGlnArgLysThrValLysCysPheAsnCysGlyI ArcGcccGcAAcTGccGcGcCcCcCGcAAGAAGGGCTGCTGGAAGTGCC
ThrAlaPr CAGGAGAG		igen igen igen igen igen igen igen igen	1126 AAGAGCAACTTCAAGGGCCCCCGGCGCATCGTCAAGTGCTTCAACTGCGGCAACTTCAAGTGCTTCAACTGCGGCAACTGCGGCAACTGCGGCAACTGCAACTGCAACTGCAACTGCAACTACAACTGCAACTACAACTACAACTACAACTACAACTACAACTACAACTACAACTACT	Qy       1072 GCCCGCGTGCTGGCCGAGGCGAGGCGATGAGGCCAACACCAGCGTGATGATGCAG 1125	Qy 1012 GGCGCCAGCCTGGAGGAGATGATGACCGCCTGCCAGGGGTGGGGGGGCCCCAGCCAAG 1071    :::	Qy 952 ACCCTGCTGGTGCAGAACGCCAACCCCCGACTGCAAGACCATCCTGCGCGCGC	Oy 892 TTCTTCAAGACCCTGCGCGCCGAGCAGAGCACCCAGGAGGTGAAGAACTGGATGACCGAC 951    :::                :::::	QY 832 GTGAGCATCCTGGACATCAAGCAGGGCCCCAAGGAGCCCTTCCGCGACTACGTGGACCGC 891	Qy 772 GACATCTACAAGCGGTGGATCATCCTGGGCCTGAACAAGATCGTGCGGATGTACAGCCCC 831 :::	OY 712 ACCAGCACCCTGCAGGAGCAGATCGCCTGGATGACCAGCAACCCCCCCATCCCCGTGGGC 771	Qy 652 GCCGGCCCATCGCCCCGGCCAGATGCGCGAGCCCCGGGGAGCCAGCGACATCGCCGGCACC 711	Qy 592 ATGCTGAAGGACACCATCAACGAGGAGGCCGCCGAGTGGGACCGCGTGCACCCCCGTGCAC 651	Qy 532 ACCCCCCAGGACCTGAACACGATGTTGAACACCGTGGGCCGCCACCAGGCCGCCATGCAG 591	QY 472 GAGGAGAAGGCCTTCAGCCCCGAGGTGATCCCCCATGTTCACCGCCCTGAGCGAGGGCGCC 531	QY 412 GGCCAGATGGTGCACCAGGCCATCAGCCCCGCACCCTGAACGCCTGGGTGAAGGTGATC 471	Qy 361 GCCGACAAGGGCAAGGTGAGCCAGAACTACCCCCATCGTGCAGAACCTGCAG 411           :::	

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..,...ernate names: core polyprotein
N;Contains: core protein p1; core protein p17; core protein p2; core protein p24; core protein p18; core protein p27; core protein p27; core protein p24; core protein p28; core protein p29; core protein p24; core p2; core protein p24; core p2; core protein p24; core p2; core p2; core p24; core p2; core p24; core p25; core p26; core p26; core p27; core p28; core p28; core p29; 
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C;Superfamil
C;Keywords:
F;1-134/Prod
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                         GluLysIleGluGluGluGlnAsnLysSerLysLysLysAlaGlnGlnAla---AlaAla
                                          GACAAGATCGAGGAGGAGCAGAACAAGTGCCAGCAGGAAGATCCAGCAGGCCGAGGCCGCC
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A;Molecule type: DNA
A;Residues: 1-478 <MUE>
A;Cross-references: UNIPROT:P03350
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                               Best I
Query
DB:
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F;133-363/Product: capsid antigen core protein p24CA #status
F;133-363/Product: capsid antigen core protein p24CA #status
F;364-377/Product: core protein p2 #status predicted <CP2>
F;378-432/Product: nucleocapsid core protein p7NC #status pre-
F;392-405/Region: zinc finger CCHC motif
F;413-426/Region: zinc finger CCHC motif
F;2/Modified site: myristylated amino end (Gly) (in mature fo
F;392,395,400,405/Binding site: zinc (Cys, Cys, His, Cys) #st
F;413,416,421,426/Binding site: zinc (Cys, Cys, His, Cys) #st
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A;Title: Nucleic acid structure and expression of the human AIDS/lymphadenopathy A;Reference number: A93355; MUID:85111157; PMID:2982104
A;Accession: A03948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Genetics:
A; Gene: gag
A; Gene: gag
C; Superfamily: AIDS-related virus gag polyprotein
C; Keywords: AIDS; blocked amino end; core protein;
F; 2-478/Product: gag precursor (assemblin) #status
F; 2-132/Product: matrix antigen core protein p17MA
F; 20-32/Region: nuclear location signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gag polyprotein - human immunodeficiency virus type 1 (isolate LV)
N;Alternate names: assemblin; core polyprotein; gag precursor
N;Contains: capsid antigen core protein p24CA; core protein p1; core proteil
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 09-Jul-2004
C;Accession: A03948
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359 1071 339 1011 319 951

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gag polyprotein - simian immunodeficiency virus SIVcpz
N;Alternate names: core polyprotein
C;Species: simian immunodeficiency virus SIVcpz
A;Note: host Pan troglodytes (chimpanzee)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-C;Accession: S09983
R;Huet, T.; Cheynier, R.; Meyerhans, A.; Roelants, G.; Wain-Hobson, S.
Nature 345, 356-359, 1990
A;Title: Genetic organization of a chimpanzee lentivirus related to HIV
A;Reference number: S09983; MUID:90259077; PMID:2188136
A;Accession: S09983
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-508 <HUE>
A;Cross-references: UNIPROT:P17282; EMBL:X52154; NID:g58866; PIDN:CAA36
C;Genetics:
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C;Superfamily: i
C;Keywords: AID
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Matches:
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C;Species: human immunodeficiency virus type 2 D205

C;Species: human immunodeficiency virus type 2 D205, HIV-2 D205

C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change

C;Accession: $08435

R;Dietrich, U.; Adamski, M.; Kreutz, R.; Seipp, A.; Kuehnel, H.;

Nature 342, 948-950, 1989

A;Title: A highly divergent HIV-2-related isolate.

A;Reference number: $08434; MUID:90081881; PMID:2594088

A;Accession: $08435
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                                                                                                                 AGCCTGTTCGGCAACGACCCCCTGAGCCAG
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---LysSerGlnGluLysLysGluGlyGluSerSerLeuTyrProProThrSerLeuLys
                                         AsnArgThrGluProThrAlaProProIleGluSerTyrGlyTyrGlnGluGluGlu---
                                                       AGCCGCCCGAGCCCACCGCCCCCCCCCGAGAGAGCTTCCGCTTCGAGGAGACCACCCCC
                                                                                                                                  AAGGGCTGCTGGAAGTGCGGCAAGGAGGGCCACCAGATGAAGGACTGCACCGAGCGCCAG
                                                                                                                                                                LysCysPheAsnCysGlyLysGluGlyHisLeuAlaArgAsnCysLysAlaProArgArg
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H.;

Ruebsamen-Waigmann,

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09-Jul-2004

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A;Status: nucleic acid sequence not sha,Molecule type: DNA
A;Residues: 1-521 <DIE>
A;Cross-references: UNIPROT:P15832; EN
A;Note: this sequence was submitted to
C;Genetics:
A;Gene: gag
C;Superfamily: AIDS-related virus gag
C;Keywords: polyprotein
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gag polyprotein - human immunodeficiency virus type 2
C;Species: human immunodeficiency virus type 2, HIV-2
C;Species: human immunodeficiency virus type 2, HIV-2
C;Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change (C;Accession: $53091
R;Becker, M.; Zorr, B.; Becker, A.; Habermehl, K.O.
submitted to the EMBL Data Library, March 1995
submitted to the EMBL Data Library, March 1995
            A;Description: Molecular and phylogenetic characterisation of A;Reference number: S53091
A;Accession: S53091
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-521 <BEC>
A;Cross-references: UNIPROT:Q76621; EMBL:Z48731; NID:g732718; C;Superfamily: AIDS-related virus gag polyprotein
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Search completed: March 11, 2005, 15:43:00 Job time: 87.7254 secs

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## **Protein Sequence Searches - February 2005**

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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-Q=/cgn2_1/USPTO_spool_p/US09475704/runat_10032005_140221_14821/app_query.fasta_1.3342
-DB=Uniprot_03 -QFMT=fastan -SUFFIX=n2p.rup -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
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-UNITS=bits -START=1 -FAD=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DCCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
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## ALIGNMENTS

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ID QSWF75

PRELIMINARY; PRT; 492 AA.

AC QSWF75,

O1-NOV-1999 (TrEMBLrel. 12, Created)

DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)

DT 01-NOV-1999 (TrEMBLrel. 26, Last annotation update)

DE Gag polyprotein.

GN Name-gag;

OS Human Immunodeficiency virus 1.

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCSI TAXID=11676;

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J. Virol. 73:4427-4432(1999).
EMBL; AF110963; AAD17037.1; -.
PIR; S49086; S49086.
HSSP; Q70622; 1HVN.
GO; GO:0019012; C:virion; IEA.
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0005198; F:structural molecule activity
GO; GO:0016032; P:viral life cycle; IEA.
InterPro; IPR000721; Gag_p24.
InterPro; IPR010999; Retrovir_matrix.
InterPro; IPR000071; Retrovir_p17.
InterPro; IPR0008916; Retrov_capsid_C.
                                                                                                                                      SEQUENCE FROM N.A.

MEDLINE=99214383; PubMed=10196340;

Novitsky V.A., Montano M.A., McLane M.F., Renjifo B., Vannberg F.,

Foley B.T., Ndung'u T.P., Rahman M., Makhema M.J., Marlink R.,

Essex M.;

"Molecular cloning and phylogenetic analysis of human immunodeficiency

virus type 1 subtype C: a set of 23 full-length clones from

Botswana.";

J. Virol. 73:4427-4432(1900)
                                                                                                                                                                                                                                                                                                                                     Q9WF69;
Q9WF69;
01-NOV-1999
01-NOV-1999
01-OCT-2003
                                                                                                                                                                                                                                                                      Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae;
NCBI_TaxID=11676;
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Name=gag;
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Best Local Similarity:
Query Match:
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InterPro; IPR001878; Znf_CCHC.
Pfam; PF00540; Gag_p17; 1.
Pfam; PF00607; Gag_p24; 1.
Pfam; PF00098; Zf-CCHC; 2.
PRINTS; PR00939; C2HCZNFINGER.
PRINTS; PR00934; HIV1MATRIX.
SMART; SM00343; ZnF_C2HC; 2.
PROSITE; PS50158; ZF_CCHC; 2.
PROSITE; PS50158; ZF_CCHC; 2.
AIDS; Core protein; Metal-binding; Polyprotein; Zinc; Zinc-finger.
SEQUENCE 492 AA; 55098 MW; C33DEDA2CB6ED800 CRC64;
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                    ACCGTGGCCACCCTGTACTGCGTGCACGAGAAGATCGAGGTCGGCGACACCAAGGAGGCC
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2599.00
99.80%
99.59%
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O9WF66;
Q9WF66;
Q9WF66;
Q1-NOV-1999 (TrEMBLrel. 12, Created)
Q1-NOV-1999 (TrEMBLrel. 26, Last sequence)
Q1-MAR-2004 (TrEMBLrel. 26, Last annotatic)
Gag polyprotein.
Name=gag;
Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Le
NCBI_TaxID=11676;
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=99214383; PubMed=10196340;
Novitsky V.A., Montano M.A., McLane M.F., Renjifo B., Vannberg F.,
Foley B.T., Ndung'u T.P., Rahman M., Makhema M.J., Marlink R.,
Essex M.;
"Molecular cloning and phylogenetic analysis of human immunodeficiency
virus type 1 subtype C: a set of 23 full-length clones from
Botswana.";
J. Virol. 73:4427-4432(1999).
EMBL; AF110962; AAD17029.1; -.
EMBL; AF110962; IHVN.
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GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0005198; F:structural molecule activity; IE;
GO; GO:0016032; P:viral life cycle; IEA.
InterPro; IPR000721; Gag_p24.
InterPro; IPR010999; Retrovir_matrix.
InterPro; IPR0009071; Retrov_capsid_C.
InterPro; IPR000916; Retrov_capsid_N.
InterPro; IPR008916; Retrov_capsid_N.
InterPro; IPR008919; Retrov_capsid_N.
InterPro; IPR001878; Znf_CCHC.
R ffam; PF00540; Gag_p17; 1.
Pfam; PF00540; Gag_p24; 1.
Pfam; PF00607; Gag_p24; 1.
Pfam; PF00098; zf-CCHC; 2.
SMART; SM00343; ZnF_C2HC; 2.
SMART; SM00343; ZnF_C2HC; 2.
ALDS; Core protein; Polyprotein.
SEQUENCE 492 AA; 55210 MW; 19657901783EFDBC CRC
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01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence
01-OCT-2003 (TrEMBLrel. 25, Last annotatic
Gag polyprotein.
Name=gag;
Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae; Le
NCBI_TaxID=11676;
SEQUENCE FROM N.A.

MEDLINE=99214383; PubMed=10196340;

Novitsky V.A., Montano M.A., McLane
Foley B.T., Ndung'u T.P., Rahman M..
Essex M.;
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R HSSP; Q70622; 1HVN.

R GO; GO:0019012; C:virion; IEA.

R GO; GO:0003676; F:nucleic acid binding; IEA.

R GO; GO:0005198; F:structural molecule activity; IER

R GO; GO:0005198; F:viral life cycle; IEA.

R GO; GO:0005198; F:viral life cycle; IEA.

InterPro; IPR000721; Gag_p24.

R InterPro; IPR000999; Retrovir_matrix.

R InterPro; IPR0009916; Retrov_capsid_C.

InterPro; IPR008919; Retrov_capsid_N.

InterPro; IPR008919; Retrov_capsid_N.

InterPro; IPR008919; Retrov_capsid_N.

InterPro; IPR001878; Znf_CCHC.

R InterPro; IPR001878; Znf_CCHC.

R Ffam; PF00540; Gag_p17; I.

R Pfam; PF00607; Gag_p24; 1.

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Gag protein.
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N [2]

SEQUENCE FROM N.A.

NOVITSKY V.A., McLane M.F., Chigwedere P., Ndung'u Chang S.-Y., Peter T., Thior I., Rybak N., Gaseits:

A Marlink R., Lee T.-H., Essex M.;

Submitted (OCT-2001) to the EMBL/GenBank/DDBJ datal Submitted (OCT-2001) to the EMBL/GenBank/DDBJ datal FMBL; AF443100; AAL34787.1; -.

R EMBL; AF443100; AAL34787.1; -.

R GO; GO:0019012; C:virion; IEA.

GO; GO:0019012; C:virion; IEA.

GO; GO:0003676; F:nucleic acid binding; IEA.

GO; GO:0003676; F:nucleic acid binding; IEA.

GO; GO:0005198; F:structural molecule activity; IEJ.

R GO; GO:0016032; P:viral life cycle; IEA.

Ffam; PF00540; Gag_D27; 1.

R Pfam; PF00540; Gag_D27; 1.

R Pfam; PF000540; Gag_D24; 1.
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( NCBI_TaxID=11676;

[1]

SEQUENCE FROM N.A.

( MEDLINE=21988475; PubMed=11991972;

( DOI=10.1128/JVI.76.11.5435-5451.2002;

( Novitsky V., Smith U.R., Gilbert P., McLane M.F., Chi Williamson C., Ndung'u T., Klein I., Chang S.-Y., Pet Foley B.T., Gaolekwe S., Rybak N., Gaseitsiwe S., Var Marlink R., Lee T.-H., Essex M.;

"Human immunodeficiency virus type 1 subtype C molecutonsensus sequence for an AIDS vaccine design?";

J. Virol. 76:5435-5451(2002).
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                                          SerLeuLysSerLeuPheGlyAsnAspProLeuSerGln
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RC STRAIN=98ZA445;

RC MEDLINE=22567157; PubMed=12680693; DOI=10.1023/A:1022378022104;

RA Hunt G.M., Papathanasopoulos M.A., Gray G.E., Tiemessen C.T.;

RT "Characterisation of near-full length genome sequences of three South

RT African human immunodeficiency virus type 1 subtype C isolates.";

RL Virus Genes 26:49-56(2003).

DR HSSP; Q70622; HYNN.

GO; GO:0019012; C:virion; IEA.

GO; GO:0005198; F:structural molecule activity; IEA.

GO; GO:0005198; F:structural molecule activity; IEA.

GO; GO:0005198; F:structural molecule activity; IEA.

DR InterPro; IPR000721; Gag_p24.

DR InterPro; IPR00099; Retrovir matrix.

DR InterPro; IPR000916; Retrovir_p17.

DR InterPro; IPR008916; Retrov-Capsid_N.

InterPro; IPR008916; Retrov-Capsid_N.

DR InterPro; IPR0011978; Znf_CCHC.

Pfam; PF00540; Gag_p17; I.

DR Pfam; PF00540; Gag_p24; 1.

DR Pfam; PF00098; zf-CCHC; 2.

DR PART; SM00343; Znf_CCHC; 2.

DR PROSITE; PS50158; ZF_CCHC; 2.

DR PROSITE; PS50158; ZF_CCHC; 2.

SMART; SM00343; Znf_CCHC; 2.

DR PROSITE; PS50158; ZF_CCHC; 2.
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Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae;
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GO; GO:0019012; C:virion; IEA.

GO; GO:0003676; F:nucleic acid binding; IEA.

GO; GO:0005198; F:structural molecule activity; IE,

GO; GO:0016032; P:viral life cycle; IEA.

Pfam; PF00540; Gag_D24; 1.

Pfam; PF00607; Gag_D24; 1.

Pfam; PF00098; zf-CCHC; 2.

PRINTS; PR00939; C2HCZNFINGER.

PRINTS; PR00934; HIVIMATRIX.

SMART; SM00343; ZnF_CCHC; 2.

PROSITE; PS50158; ZF_CCHC; 2.

PROSITE; PS50158; ZF_CCHC; 2.

SMART; Core protein; Metal-binding; Polyprotein; Zi

AIDS; Core protein; Metal-binding; Polyprotein; Zi

SEQUENCE 492 AA; 55196 MW; CFDAE0D5BA9F4EE9 CR
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MEDLINE=21565558; PubMed=11709097; DOI=
van Harmelen J., Williamson C., Kim B.,

Abdool Karim S.S., McCutchan F.;

"Characterization of full-length HIV ty
South Africa.";

AIDS Res. Hum. Retroviruses 17:1527-153

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Abdool Karim S.S., McCutchan F.;
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ
EMBL; AY043175; AAL05325.1; -.
PIR; S49086; S49086.
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n B., Morris L., Carr J.,
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Abdool Karim S.S., McCutchan F.;
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ datal
REMBL; AY043176; AAL05334.1; -.
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REMBL; AY043176; Finucleic acid binding; IEA.
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GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
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                                 CTGGAGGAGATGATGACCGCCTGCCAGGGCGTGGGCGCCCCAGCCACAAGGCCCGCGTG
                                                                                                               LeuAlaGluAlaMetSerGlnAlaAsnAsnIleAsnIleMetMetGlnLysSerAsnPhe
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REMBL; AF544010; AAO16234.1; -.

REMBL; AF544010; C:virion; IEA.

GO; GO:0019012; C:virion; IEA.

GO; GO:0003676; F:nucleic acid binding; IEA.

GO; GO:0005198; F:structural molecule activity; IEA

GO; GO:0005198; F:structural molecule activity; IEA

GO; GO:0016032; P:viral life cycle; IEA.

InterPro; IPR0010721; Gag_p24.

InterPro; IPR001071; Retrovir_p17.

R InterPro; IPR0008916; Retrov_capsid_C.

InterPro; IPR001878; Znf_CCHC.

R InterPro; IPR001878; Znf_CCHC.

R Ffam; PF00540; Gag_p17; 1.

R Pfam; PF000540; Gag_p24; 1.

Pfam; PF00098; zf-CCHC; 2.

R Pfam; PF00098; zf-CCHC; 2.

R PSS0158; ZF_CCHC; 2.

AIDS; Core protein; Folyprotein.

SEQUENCE 492 AA; 55221 MW; B1922020A1AE861B CRC
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Q8AFW4;
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Gag protein.
Name=gag;
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SEQUENCE FROM N.A.

MEDLINE=22525961; PubMed=12639249; DOI=10.1089/088922203762688649;

Williamson C., Morris L., Maughan M.F., Ping L.-H., Dryga S.A.,

Thomas R., Reap E.A., Cilliers T., van Harmelen J., Pascual A.,

Ramjee G., Gray G., Johnston R., Karim S.A., Swanstrom R.;

Roman G., Gray G., Johnston R., Karim S.A., Swanstrom R.;

"Characterization and selection of HIV-1 subtype C isolates for us
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A Novitsky V.A., McLane M.F., Chigwedere P., Ndung'u Chang S.-Y., Peter T., Thior I., Rybak N., Gaseits: A Marlink R., Lee T.-H., Essex M.;

A Chang S.-Y., Peter T., Thior I., Rybak N., Gaseits: Submitted (OCT-2001) to the EMBL/GenBank/DDBJ datal EMBL; AF443087; AAL34670.1; -.

R MSSP; Q70622; 1HVN.

R GO; GO:0019012; C:virion; IEA.

GO; GO:0019012; C:virion; IEA.

GO; GO:0003676; F:nucleic acid binding; IEA.

GO; GO:0005198; F:structural molecule activity; IEJ

R GO; GO:0016032; P:viral life cycle; IEA.

Ffam; PF00540; Gag_p17; 1.

Pfam; PF00607; Gag_p24; 1.

R Pfam; PF00607; Gag_p24; 1.

R Pfam; PF00098; zf-CCHC; 2.

PRINTS; PR00939; zf-CCHC; 2.

R PRINTS; PR00934; TIVIMATRIX.

R PRINTS; PR00343; ZnF_C2HC; 2.

R PROSITE; PS50158; ZF_CCHC; 2.

AIDS; Core protein; Metal-binding; Polyprotein; Zir

AIDS; Core protein; Metal-binding; Polyprotein; Zir

AIDS; Core protein; Metal-binding; Polyprotein; Zir
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SEQUENCE FROM N.A.

MEDLINE=21988475; PubMed=11991972;

DOI=10.1128/JVI.76.11.5435-5451.2002;

Novitsky V., Smith U.R., Gilbert P., McLane M.F., Chigwed, Novitsky V., Smith U.R., Klein I., Chang S.-Y., Peter T. Foley B.T., Gaolekwe S., Rybak N., Gaseitsiwe S., Vannber, Marlink R., Lee T.-H., Essex M.;

"Human immunodeficiency virus type 1 subtype C molecular consensus sequence for an AIDS vaccine design?";

J. Virol. 76:5435-5451(2002).
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RESULT 12
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AC Q8UT71;
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DT 01-MAR-2002 (
DT 01-MAR-2004 (
DE Gag protein.
GN Name=gag;
OS Human immunoc
OC Viruses; Reti
OX NCBI TaxID=11
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RN MEDLINE=21986
RX DOI=10.1128/C
RA NOVITSKY V.,
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RA MARTINK R., I
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RA GO; GO:001501
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DR Pfam; PF00050
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consensus sequence for an AIDS vaccine design?";

L J. Virol. 76:5435-5451(2002).

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P SEQUENCE FROM N.A.

Novitsky V.A., McLane M.F., Chigwedere P., Ndung's Chang S.-Y., Peter T., Thior I., Rybak N., Gaseit Amarlink R., Lee T.-H., Essex M.;

Submitted (OCT-2001) to the EMBL/GenBank/DDBJ dat EMBL; AF443099; AAL34778.1; -.

R HSSP; P24736; INCP.

R GO; GO:0019012; C:virion; IEA.

R GO; GO:0019012; C:virion; IEA.

R GO; GO:0005198; F:structural molecule activity; 1

R GO; GO:0016032; P:viral life cycle; IEA.

R GO; GO:0016032; P:viral life cycle; IEA.

R Pfam; PF000540; Gag_p17; 1.

R Pfam; PF00098; zf-CCHC; 2.

R PROSITE; PS50158; ZF_CCHC; 2.
                                                                                                                                                            SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=21988475; PubMed=11991972;

DOI=10.1128/JVI.76.11.5435-5451.2002;

Novitsky V., Smith U.R., Gilbert P., McLane M.F., Chigwed, Milliamson C., Ndung'u T., Klein I., Chang S.-Y., Peter T Foley B.T., Gaolekwe S., Rybak N., Gaseitsiwe S., Vannber, Marlink R., Lee T.-H., Essex M.;

"Human immunodeficiency virus type 1 subtype C molecular | Consensus sequence for an AIDS vaccine design?";

J. Virol. 76:5435-5451(2002).
                                                                                                                                                                                                                                                                   Human immunodeficiency virus 1.
Viruses; Retroid viruses; Retroviridae;
NCBI_TaxID=11676;
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J. Virol. 76:5435-5451(2002).

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SEQUENCE FROM N.A.

Novitsky V.A., McLane M.F., Chigwedere P., Ndung Chang S.-Y., Peter T., Thior I., Rybak N., Gaseit Marlink R., Lee T.-H., Essex M.;

Submitted (OCT-2001) to the EMBL/GenBank/DDBJ date EMBL; AF443101; AAL34796.1; -.

REMBL; AF443101; AAL34796.1; -.

RESP; Q70622; 1HVN.

GO; GO:0003676; F:nucleic acid binding; IEA.
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Q8UT53;
01-MAR-2002
01-MAR-2002
01-MAR-2004
Gag protein.
                                                                                                                                                        MEDLINE=21988475; PubMed=11991972;
DOI=10.1128/JVI.76.11.5435-5451.2002;
DOI=10.1128/JVI.76.11.5435-5451.2002;
Novitsky V., Smith U.R., Gilbert P., McLane M.F., Chigwedere Williamson C., Ndung'u T., Klein I., Chang S.-Y., Peter T., T Foley B.T., Gaolekwe S., Rybak N., Gaseitsiwe S., Vannberg F. Marlink R., Lee T.-H., Essex M.;
"Human immunodeficiency virus type 1 subtype C molecular phyl consensus sequence for an AIDS vaccine design?";
J. Virol. 76:5435-5451(2002).
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Viruses; Retroid viruses; Retroviridae;
NCBI_TaxID=11676;
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GO; GO:0016032; P:viral life cycle; IEA.
Pfam; PF00540; Gag_p17; 1.
Pfam; PF00607; Gag_p24; 1.
Pfam; PF00098; zf-CCHC; 2.
SMART; SM00343; ZnF_C2HC; 2.
PROSITE; PS50158; ZF_CCHC; 2.
AIDS; Core protein; Polyprotein.
SEQUENCE 492 AA; 55087 MW; 9B80F1A1426E80C9 CRC6.
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Gupta R.M., Prasad V., Singh B., Seth P.;
Submitted (JUL-2002) to the EMBL/GenBank/D.
EMBL; AF533131; AAP87971.1; -.
HSSP; Q70622; 1HVN.
GO; GO:0019012; C:virion; IEA.
GO; GO:0003676; F:nucleic acid binding; IE.
GO; GO:0005198; F:structural molecule acti-
GO; GO:0016032; P:viral life cycle; IEA.
InterPro; IPR000721; Gag_p24.
InterPro; IPR010999; Retrovir_matrix.
InterPro; IPR010999; Retrovir_p17.
InterPro; IPR0008916; Retrov_capsid_C.
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Q7SLX7;
01-OCT-2003
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01-MAR-2004
Gag protein.
                                                                                                                                                                                  Human immunodeficiency
Viruses; Retroid viruse
NCBI_TaxID=11676;
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Name=gag;
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InterPro; IPR001878; Znf_CCHC.
Pfam; PF00540; Gag_p17; I.
Pfam; PF00607; Gag_p24; 1.
Pfam; PF00098; zf-CCHC; 2.
SMART; SM00343; Znf_CCHC; 2.
PROSITE; PS50158; Zf_CCHC; 2.
AIDS; Core protein; Polyprotein.
SEQUENCE 491 AA; 54815 MW; 36CD9A56
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      AAGCGGTGGATCATCCTGGGCCTGAACAAGATCGTGCGGATGTACAGCCCCGTGAGCATC
                                                                                    CTGGACAAGATCGAGGAGGAGGAGAACAAGTGCCAGCAGAAGATCCAGCAGGCCGAGGCCC
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Gupta R.M., Prasad V., Singh B., Seth P.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ da:
EMBL; AF533135; AAP87975.1; -.
HSSP; Q70622; 1HVN.
GO; GO:0019012; C:virion; IEA.
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0005198; F:structural molecule activity;
GO; GO:0016032; P:viral life cycle; IEA.
InterPro; IPR000721; Gag_p24.
InterPro; IPR010999; Retrovir_matrix.
InterPro; IPR000071; Retrovir_b17.
InterPro; IPR0008916; Retrov_capsid_C.
                                                                                                                                                             Viruses; Retroid vi
NCBI_TaxID=11676;
[1]
SEQUENCE FROM N.A.
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Q7SLX3;
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Q1-MAR-2004
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InterPro; IPR001878; Znf_CCHC.
Pfam; PF00540; Gag_p17; 1.
Pfam; PF000607; Gag_p24; 1.
Pfam; PF00098; zf-CCHC; 2.
SMART; SM00343; ZnF_C2HC; 2.
PROSITE; PS50158; ZF_CCHC; 2.
AIDS; Core protein; Polyprotein.
SEQUENCE 492 AA; 55105 MW; 78697BC7E49D3CD3
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Search completed: March 11, 2005, 15:39:19 Job time : 285.42 secs

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Copyright (c) 1993 - 2005 Compugen Ltd.
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AX455887 Sequence
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#### ALIGNMENTS

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                                                                                                                                                    GGCCCCCGGCGCATCGTCAAGTGCTTCAACTGCGGCAAGGAGGGCCACATCGCCCGCAAC
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Best Local Similarity
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Microparticles for delivery of the heterologous nucleic acids Patent: WO 0226209-A 63 04-APR-2002;
CHIRON CORPORATION (US)
Location/Qualifiers
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Human immunodeficiency virus 1
Viruses; Retroid viruses; Retroviridae;
lentivirus group.
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 GTGCACCAGGCCATCAGCCCCGCACCCTGAACGCCTGGGTGAAGGTGATCGAGGAGAAGA
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                                                  GCCGACAAGGGCAAGGTGAGCCAGAACTACCCCATCGTGCAGAACCTGCAGGGCCAGATG
                                                                     GCCGACAAGGGCAAGGTGAGCCAGAACTACCCCATCGTGCAGAACCTGCAGGGCCAGATG
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/mol_type="unassigned DNA"
/db_xref="taxon:11676"
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                                                                                                                                                          Submitted (16-NOV-2002) Medicine, Duke University Medical Center, 112 RPIII, LaSalle Street, Durham, NC 27710, USA Location/Qualifiers
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AIDS Res. Hum. Retroviruses 19 (9), 817-823 (2003)
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Gao,F., Li,Y., Decker,J.M., Bibollet-Ruche,F., Rodenburg,C.M., Chen,Y., Shaw,D.R., Allen,S., Musonda,R., Shaw,G.M., Zajac,A.J.
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TACAAGCGGTGGATCATCCTGGGCCTGAACAAGATCGTGCGGATGTACAGCCCCGTGAGC
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CGKEGHIARNCRAPRKKGCWKCGKEGHQMKDCTERQANFLGKIWPSHKGRPGNFLQNR
PEPTAPPAESFRFEETTPAPKQESKDREALTSLKSLFGSDPLSQ"
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Qy 1021 CTGGAGGAGATGATGACCGCCTGCCAGGCGTGGGCGGCCCAGCCACAAGGCCCGCGTG 1080	ō
958 GTGCAGAACGCCAACCCCGACTGCAAGACCATCCTGCGCGCCCTGGGCCCCGGCGCCCAGC 1	/ """ T ' Y PO"
898 ACCTTGCGCGGAGAGCAGAGCACCCAGGAGGTGAAGAACTGGATGACCGACACCC	Bource
901 ACCCTGCGCGCGAGCAGAGCACCCCAGGAGGTGAAGAACTGGATGACCGACACCCTGCTG 9	JOURNAL Patent: WO 0204493-A 99 17-JAN-2002; CHIRON CORPORATION (US) ; University of Stellenbosch (ZA)
QY 841 CTGGACATCAAGCAGGGCCCCAAGGAGCCCTTCCGCGACTACGTGGACCGCTTCTTCAAG 900	AUTHORS zur Megede, J., Barnett, S.W., Engelbrecht, S. and van Rensburg, E. TITLE Polynucleotides encoding antigenic hiv type c polypeptides, polypeptides and uses thereof
QY 781 AAGCGGTGGATCATCCTGGGCCTGAACAAGATCGTGCGGATGTACAGCCCCGTGAGCATC 840	URCE ORGANISM
QY 721 CTGCAGGAGCAGATCGCCTGGATGACCAGCAACCCCCCATCCCCGTGGGCGACATCTAC 780	ON Sequence 99 from Patent WO0204493.  N AX455983  AX455983.1 GI:21714967
OY 661 ATCGCCCCGGCCAGATGCGCGAGCCCCGCGGCAGCATCGCCGGCACCACCAGCACC 720	3YA55083 1A01 1
QY 601 GACACCATCAACGAGGAGGCCGCCGAGTGGGACCGCCGTGCACGCCGGCCCC 660	QY 1435 ACCAGCCTGAAGAGCCTGTTCGGCAACGACCCCCTGAGCCAGTAA 1479
CTGAAG 6	QY 1375 TTCCGCTTCGAGGAGACCACCCCCGGCCAGAAGCAGGAGCAAGGACCGCGAGACCCTG 1434
QY 481 GCCTTCAGCCCCGAGGTGATCCCCATGTTCACCGCCCTGAGCGAGGGGCGCCACCCCCCAG 540	QY 1315 GGCCGCCCGGCAACTTCCTGCAGAGCCGCCCGCGCGCGCCCCCCCC
63-63	QY 1255 ATGAAGGACTGCACCGAGCGCCAGGCCAACTTCCTGGGCAAGATCTGGCCCAGCCACAAG 1314
QY 361 GCCGACAAGGGCAAGGTGAGCCAGAACTACCCCATCGTGCAGAACCTGCAGGGCCAGATG 420	QY 1195 CGCAACTGCCGCCCCCCCCCAAGAAGGGCTGCTGGAAGTGCGGCAAGGAGGGCCACCAG 1254
OY 301 CTGGACAAGATCGAGGAGGAGCAGAACAAGTGCCAGCAGAAGATCCAGCAGGCCGAGGCC 360	QY 1135 TTCAAGGGCCCCCGGCGATCGTCAAGTGCTTCAACTGCGGCAAGGAGGGCCACATCGCC 1194
QY 241 ACCGTGGCCACCCTGTACTGCGTGCACGAGAAGATCGAGGTCCGCGACACCAAGGAGGCC 300	QY 1078 GTGCTGGCCGAGGCCAGGCCAGGCCAACACCAGCGTGATGCAGAAGAGCAAC 1134
QY 181 ATCCGCCAGCTGCACCCCGCCCTGCAGACCGGCAGCGAGGAGCTGAAGAGCCTGTTCAAC 240	QY 1018 AGCCTGGAGGAGATGATGACCGCCTGCCAGGGCGTGGGCGGCCCAGCCACAAGGCCCGC 1077
QY 121 CTGGAGAAGTTCGCCCTGAACCCCGGCCTGCTGGAGACCAGCGAGGGGCTGCAAGCAGATC 180	QY 958 CTGGTGCAGAACGCCAACCCCGACTGCAAGACCATCCTGCGCGCTCTCGGCCCCGGCGCC 1017
QY 61 CTGCGCCCCGGCGGCAAGAAGTGCTACATGATGAAGCACCTGGTGTGGGCCAGCCGCGAG 120	QY 898 AAGACCCTGCGCGCCGAGCAGAGCACCCCAGGAGGTGAAGAACTGGATGACCGACACCCTG 957
QY 1 ATGGGCGCCCGCGCCAGCATCCTGCGCGGCAAGCTGGACGCCTGGGAGCGCATCCGC 60	QY 838 ATCCTGGACATCAAGCAGGGCCCCAAGGAGGCCCTTCCGCGACTACGTGGACCGCTTCTTC 897
Best Local Similarity 93.0%; Pred. No. 3.1e-130; Matches 1389; Conservative 0; Mismatches 87; Indels 18; Gaps 3;	781 TACAAGCGCTGGATCATCCTGGGCCTGAACAAGATCGTGCGCATGTACAGCCCCGTGAGC 840

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1 ATGGCCCCCGCCCAGCATCCTGCGCCGCGGCAAGCTGGACGCCTGGGAGCCGATCCGC 60	atch cal Similaı 1393; Cor	CHIRON CORPORATION (US); University of Stellenbosch (ZA)  Location/Qualifiers  rce 1. 1494  /organism="synthetic construct" /mol_type="unassigned DNA" /db_xref="taxon:32630" /note="HIV Type C Gag optimized"	zur Megede, J., Barnett, S.W., Engelbrecht, S. and van Rensburg, E. Polynucleotides encoding antigenic hiv type c polypeptides, polypeptides and uses thereof	synthetic construct M synthetic construct other sequences; artificial sequences.	AX455935 1494 bp DNA linear PAT 06-JUL-2002 N Sequence 51 from Patent WO0204493. AX455935 AX455935.1 GI:21714919		1426 GAGACCCTGACCAGCCTGAAGAGCCTGTTCGGCAACGACCCCCTGAGCCAGTAA 1479 	1378 CGCTTCGAGGAGACCACCCCCGGCCAGAAGCAGGAGAGCAAGGACCGC 1425	1318 CGCCCGGCAACTTCCTGCAGAGCCGCCCCGAGCCCACCGCCCCCCCC	1258 AAGGACTGCACCGAGCGCCAGGCCAACTTCCTGGGCAAGATCTGGCCCAGCCACAAGGGC 1317	1198 AACTGCCGCGCCCCCGCAAGAAGGGCTGCTGGAAGTGCGGCAAGGAGGGCCACCAGATG 1257 	1138 AAGGGCCCCCGGCGCATCGTCAAGTGCTTCAACTGCGGCAAGGAGGGCCACATCGCCCGC 1197 	081 CTGGCCGAGGCGATGAGCCAGGCCAACACCAGCGTGATGATGCAGAAGAGCAACTTC 11 	1018 CTGGAGGAGATGATGACCGCCTGCCAGGGCGTGGGCGGCGCCCAGCCACAAGGCCCGCGTG 1077
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Oy  301 CTGGACAAGATCGAGGAGGAGCAGAACAAGTGCCAGCAGAAGATCCAGCAGGCCGAGGCC	Db 181 ATGAAGCAGCTGCAGCCCGCCCTGCAGACCGGCACCCGAGGAGCTGCGAGCCTGTACAAC 240  QY 241 ACCGTGGCCACCCTGTACTGCGTGCACGAGGAAGATCGAGGTCCGCGACACCAAGGAGGCC 300	121 CTGGAGAAGTTCGCCCTGAACCCCGGCCTGCTGGAGACCAGCGAGGGCTGCAAGCAGATC 18	Oy  1 ATGGGCGCCGCGGCAGCATCCTGCGGCGGCAAGCTGGACGCCTGGGAGCGCATCCGC 60	жа Ма	/organism="synthetic construct" /mol_type="unassigned DNA" /db_xref="taxon:32630" /note="synthetic Gag of HIV strain AF110967"	٠ ٧	zur M Polyn Polyp	OURCE ORGANISM	DEFINITION Sequence 4 from Patent WO0204493. ACCESSION AX455888 VERSION AX455888.1 GI:21714881		QY 1420 GACCGCGAGACCCTGACCAGCCTGAAGAGCCTGTTCGGCAACGACCCCCTGAGCCAGTAA 1479	QY 1360 CCCCCGCCGAGAGCTTCCGCTTCGAGGAGACCACCCCCGGCCAGAAGCAGGAGAGAGCAAG 1419	QY       1321 CCCGGCAACTTCCTGCAGAGCCGCC
8 8 8 8 8	S & & B	5 & B &	B & B &	Q	D Qy	Qу	Oy Db	Qy	Db Qy	Db Qy	D Q	D Q	Qy dg
378 CCCCCCGAGAGCTTCCGCTTCGAGGAGCCACCCCCCCAAGCAGGAGCCCAAG 420 GACCGCGAGACCCTGACCAGCCTGAAGAGCCTGTTCGGCAACGACCCC	B AAGGACIGCACCGAGCGCCAAGGCCAACITCCIGGCAAAGAICIGGCCAAGCACACACACACACACACAC	198 AACTGCCGCGCCCCCCCCAAGAAGGACGCTGCTGGAAGTGCCGCAAGGAGGACGACCAGATG	078 CTGGCCGAGGCGATGAGCCAGGCCAACAGCGTGAACATCATGATGCAGAAGAGCAACTTC  138 AAGGGCCCCCGGCGCATCGTCAAGTGCTTCAACTGCGGCAAGGAGGGCCACATCGCCCGC  118 AAGGGCCCCCGGCGCATCGTCAAGTGCTTCAACTGCGGCAAGGAGGGCCACATCGCCCAAG  118 AAGGGCCCCCGGCGCAACGTCAAGTGCTTCAACTGCGGCAAGGAGGGCCACATCGCCCAAG	AGGAGATGATGACCGCCTGCCAGGGCGTGGGCGGCCCAGACACAGGCCCCAGAGAAGACCCCCAGAGATGATGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAG	961 GTGCAGAACGCCAACCCCGACTGCAAGACCATCCTGCGCGCTCTCGGCCCCGGCGCCCAGC 1020 	901 ACCCTGCGCGCGAGCAGAGCACCCAGGAGGTGAAGAACTGGATGACCGACACCCCTGCTG 960 	841 CTGGACATCAAGCAGGGCCCCAAGGAGCCCCTTCCGCGACTACGTGGACCGCCTTCCTT	781 AAGCGGTGGATCATCCTGGGCCTGAACAAGATCGTGCGGATGTACAGCCCCCGTGAGCATC 840	721 CTGCAGGAGCAGATCGCCTGGATGACCAGCAACCCCCCATCCCCGTGGGCGACATCTAC 780	661 ATCGCCCCCGGCCAGATGCGCGAGCCCCGCGGCAGCAGCACCAGCACCAGCACCAGCACC 720	601 GACACCATCAACGAGGAGGCCGCCGAGTGGGACCGCGTGCACCCCGTGCACGCCGGCCCC 660	541 GACCTGAACACGATGTTGAACACCGTGGGCGGCCACCAGGCCGCCATGCAGATGCTGAAG 600	481 GCCTTCAGCCCCGAGGTGATCCCCCATGTTCACCGCCCTGAGCGAGGGGCGCCACCCCCCAG 540

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                                                                                                         GCCTTCAGCCCCGAGGTGATCCCCCATGTTCACCGCCCTGAGCGAGGGGGCGCCACCCCCAG
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/mol_type="unassigned DNA"
/db_xref="taxon:11676"
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Viruses; Retroid viruses; Retro
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Microparticles for delivery of the heterologous nucleic acids Patent: WO 0226209-A 68 04-APR-2002;
CHIRON CORPORATION (US)
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/mol_type="unassigned DNA"
/db_xref="taxon:11676"
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Modifications of hiv env, gag, and po genetic immunization

Patent: WO 0232943-A 168 25-APR-2002;
GOVERNMENT OF THE UNITED STATES (US)
Location/Qualifiers
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                             CTGAAGCCCGGCGCAAGAAGCACTACATGATGAAGCACCTGGTGTGGGCCAGCCGCGAG
                                              CTGCGCCCCGGCGGCAAGAAGTGCTACATGATGAAGCACCTGGTGTGGGCCCAGCCGCGAG
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
                                                                                                                                                                                                          note="plasmid pVR1012x/s containing"
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Pred. No. 3.5e-123;
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9 0	1021 CTGGAGGAGATGATGACCGCCTGCCAGGGCGTGGGCGGCGGCCACAAGGCCCGCGTG 10
99	961 GTGCAGAACGCCAACCCCGACTGCAAGACCATCCTGCGCGCGC
839	901 ACCCTGCGCGCGAGCAGAGCACCCAGGAGGTGAAGAACTGGATGACCGACACCCTGCTG 96
779	841 CTGGACATCAAGCAGGCCCCAAGGAGCCCTTCCGCGACTACGTGGACCGCTTCTTCAAG 90
140	781 AAGCGGTGGATCATCCTGGGCCTGAACAAGATCGTGCGGATGTACAGCCCCGTGAGCATC 84
80	721 CTGCAGGAGCAGATCGCCTGGATGACCAGCAACCCCCCCATCCCCGTGGGCGACATCTAC 78
99	661 ATCGCCCCCGGCCAGATGCGCGAGCCCCGCGGCAGCACCAGCACCCACC
539	601 GACACCATCAACGAGGAGGCCGCCGAGTGGGACCGCGTGCACCCCGTGCACGCCGGCCCC 66
479	541 GACCTGAACACGATGTTGAACACCGTGGGCCGCCAGGCCAGGCCATGCAGATGCTGAAG 600
19	481 GCCTTCAGCCCCGAGGTGATCCCCCATGTTCACCGCCCTGAGCGAGGGGCGCCACCCCCCAG 540
159	421 GTGCACCAGGCCATCAGCCCCCGCACCCTGAACGCCTGGGTGAAGGTGATCGAGGAGAAG 480
299	361 GCCGACAAGGGCAAGGTGAGCCAGAACTACCCCATCGTGCAGAACCTGCAGGGCCAGATG 42 
239	301 CTGGACAAGATCGAGGAGGAGCAGAACAAGTGCCAGCAGAAGATCCAGCAGGCCGAGGCC 36 
179	241 ACCGTGGCCACCCTGTACTGCGTGCACGAGAAGATCGAGGTCCGCGACACCAAGGAGGCC 300 
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059	2000 CTGGAGCGCTTCGCCCTGGACCCCGGCCTGCTGGAGACCAGCGAGGGCTGCAAGCAGATC 2

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Patent: WO 0232943-A 174 25-APR-2002;
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AX427936.1 GI:21538023
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="plasmid pVR1012x/s containing HIV genes"
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The genome of the hiv-1 inter-subtype (c/b') and use thereof
Patent: WO 0136614-A 2 25-MAY-2001;
Geneart GMBH Gessellschaft fuer angewandte Boitechnologie (DE)
Shao, Yiming (CN)
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Sequence 2 from Patent WO0136614.
AX149648 AX149648.1 GI:14348047
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Human immunodeficiency virus
Viruses; Retroid viruses; Retroviridae;
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                                                                                                                  GCCTTCAGCCCCGAGGTGATCCCCATGTTCAGCGCCCTGAGCGAGGGCGCCACCCCCAG
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/mol_type="unassigned DNA"
/db_xref="taxon:12721"
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Pred. No. 2.2e-121;
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Synthetic construct of AF201927
AF201927.1 GI:724870
synthetic construct other sequences; artificial sequences.

1 (bases 1 to 1509)

zur Megede, J., Chen, M.C., Doe, B., Schaefer, M., Greer, C.E., Selby, M., Otten, G.R. and Barnett, S.W.
Increased expression and immunogenicity of sequence-modificimmunodeficiency virus type 1 gag gene
                                                                                                                                        synthetic construct
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    GTGGAGGAGAAGGCCTTCAGCCCCGAGGTGATCCCCATGTTCAGCGCCCTGAGCGAGGGC
                                                                                     ATCGAGGAGAAGGCCTTCAGCCCCGAGGTGATCCCCCATGTTCACCCGCCTGAGCGAGGGC
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/protein_id="AAF43628.1"
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/translation="MGARASVLSGGELDKWEKIRLRPGGKKKYKLKHIVWASRELERF
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AVNPGLLETSEGCRQILGQLQPSLQTGSEELRSLYNTVATLYCVHQRIDVKDTKEALE
KIEEEQNKSKKKAQQAAAAAGTGNSSQVSQNYPIVQNLQGQWVHQAISPRTLNAWVKV
VEEKAFSPEVIPMFSALSEGATPQDLNTMLNTVGGHQAAMQMLKETINEEAAEWDRVH
PVHAGPIAPGQMREPRGSDIAGTTSTLQEQIGWMTNNPPIPVGEIYKRWIILGLNKIV
RMYSPTSILDIRQGPKEPFRDYVDRFYKTLRAEQASQDVKNWMTETLLVQNANPDCKT
ILKALGPAATLEEMMTACQGVGGPGHKARVLAEAMSQVTNPATIMMQRGNFRNQRKTV
KCFNCGKEGHTARNCRAPRKKGCWRCGREGHQMKDCTERQANFLGKIWPSYKGRPGNF
KCFNCGKEGHTARNCRAPRKKGCWRCGREGHQMKDCTERQANFLGKIWPSYKGRPGNF
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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Pred. No. 2e-120;
Mismatches 13
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Adm73758 HIV-1 p01
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85.2	85.4	85.4	86.3	86.3	86.3	86.3	87.1	87.1	87.1	87.1	88.9	88.9	88.9	91.1	96.3	98.8	98.9	98.9	98.9	99.6	99.6	99.6	99.6	99.7
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Aaa51626 HIV codon	Adm73763 HIV-1 pol	Abl39958 Synthetic		Abl39954 Synthetic		Aaa51610 HIV synth	Adm73785 HIV-1 pol	Ab139972 Synthetic	Adm73833 HIV-1 pol	Abl40020 Synthetic	Adc13235 DNA of HI	DNA of	DNA of	DNA		Aa144552 HIV-1 p55	Adm73762 HIV-1 pol	Abl39957 Synthetic	Aaa51625 HIV codon	Adc13278 DNA of HI	Aca03590 Synthetic	Adc13279 DNA of HI	Aca03591 Synthetic	Adc13280 DNA of HI

#### RESULT 1 AAA51609 XX XX AC AAA5 AC AAA5 XX AC AAA5 XX AC AAA5 XX DT 31-C XX Gag; XX Gag; XX GAG; XX FT CDS AAA51609 standard; DNA; 1479 HIV synthetic Gag polynucleotide. 31-OCT-2000 AAA51609; (first entry) BP.

ALIGNMENTS

; expression cassette; antigenic; type C; HIV; Env; synthetic; immunization; packaging cell line; antigen presentation; ss.

Synthetic. Human immunodeficiency virus; type C strain AF110965

/product= "Synthetic\_Gag"
/note= "Codon usage pattern was modified and inhibitory
elements (INS) and RRE sites were inactivated resulting 5 Location/Qualifiers 1. .1479 /\*tag= improved expression"

### WO200039304-A2

### 06-JUL-2000.

30-DEC-1999; 99WO-US031273

31-DEC-1998; 01-SEP-1999; 98US-0114495P. 99US-0152195P.

## (CHIR ) CHIRON CORP.

Barnett S, Zur Megede ū

# WPI; 2000-452401/39. P-PSDB; AAY96943.

Polynucleotide encoding antigenic type C HIV Gag polypeptide or a HIV Env polypeptide and the polypeptide useful for immunizing a mammal especially human against HIV.

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Matches 1479; Conserv
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Pred. No. 3.2e-185;
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CTGAAGAGCCTGTTCGGCAACGACCCCCTGAGCCAGTAA 1479
                                                                                                                      TTCGAGGAGACCACCCCGGCCAGAAGCAGGAGCAAGGACCGCGAGACCCTGACCAGC
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RESULT 2
AAL44548
ID AAL44548 standard; DNA; 1479 BP.

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AC AAL44548;
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AC AAL44548;
XX
DT 29-AUG-2003 (revised)
DT 08-NOV-2002 (first entry)
XX
HIV-1 p55gag polypeptide coding sequence 1.
XX
KW HIV; ds; vaccine; gene; immune response; microparticle;
XW adsorbent surface; poly(alpha-hydroxy acid); polyhydroxy butyric acid;
XW adsorbent surface; polyorthoester; polycyanoacrylate; detergent;
XW polycaprolactone; polyorthoester; polycyanoacrylate; detergent;
XW submicron emulsion; viral infection; bacterial infection;
XX
YX
PN parasitic infection; HIV-1 p55gag polypeptide.
XX
PN WO200226209-A2.
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PN WO200226209-A2.
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PS 28-SEP-2001; 2001WO-US030540.
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28-SEP-2000; 2000US-0236105P.
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Best Local Similarity
Matches 1479; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a method of raising an immune response in a host animal. The method of the invention comprises administering a microparticle that has an adsorbent surface to which a first biologically active macromolecule (e.g. a nucleic acid) has been adsorbed. The microparticle comprises a polymer microparticle of poly(alpha-hydroxy acid), a polyhydroxy butyric acid, a polycaprolactone, a polyorthoester, a polycyanoacrylate, a detergent, and submicron emulsion. The method/microparticle of the invention is useful for immunising a host animal against viral, bacterial or parasitic infections. The present DNA sequence encodes a HIV-1 p55gag polypeptide. (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A microparticle to which a biologically active macromolecule is adsorbed, for use as a vaccine composition to treat viral, bacterial or parasitic infections, comprises a polymer microparticle, a detergent and a submicron emulsion.
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Ulmer J, Dubensky TW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1479 BP; 325 A; 529 C; 463 G; 162 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim
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Pred. No. 3.2e-185;
Indels 0; October 1888;
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                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an expression cassette comprising a polynucleotide sequence encoding an HIV Pol polypeptide. The invention also relates to a recombinant expression system for use in a host cell comprising an expression cassette, where the polynucleotide sequence further comprises control elements capable of driving expression in the selected host cell, a cell comprising an expression cassette where the polynucleotide sequence further comprises control elements compatible with the expression in the cell and a composition for generating an immunological response, comprising an expression cassette. The expression cassette and the methods of the invention are useful in eliciting an immune response, in DNA immunisation, in generation of packaging cell lines and in producing HIV Type C proteins. This sequence represents an HIV-1 polynucleotide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1479 BP; 325
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) BARNETT S W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JUL-2001; 2001US-0303192P.
31-AUG-2001; 2001US-0316860P.
16-JAN-2002; 2002US-0349871P.
                                                                                          Sequence
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16-JAN-2002;
The invention relates to a novel expression cassette comprising a polynucleotide sequence encoding a polypeptide including an HIV Gag, Int, Nef, pl5RnaseH, Pol, Tat, Prot, or Rev polypeptide. The novel expression cassette can be used to treat HIV type C by gene therapy cused in the development of a vaccine. The gene delivery vector is administered intramuscularly, intramucosally, intranasally, subcutaneously, intradermally, transdermally, intravaginally, intrarectally, orally or intravenously. The expression cassette is us
                                                                                                    New expression cassette comprising a polynucleotide sequence encoding polypeptide including an HIV Gag, Env, Int, Nef, p15RnaseH, Pol, Tat, Prot, or Rev polypeptide, useful for immunization, or generating packaging cell lines.
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16-JAN-2002; 2002US-0349728P.
16-JAN-2002; 2002US-0349793P.
16-JAN-2002; 2002US-0349871P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunogenic HIV polypeptide; human immunodeficiency virus; HIV; vaccine; gene therapy; packaging cell line; humoral immune response; cellular immune response; gene delivery vector; DNA immunisation; ds.
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5

synthetic polynucleotides encoding

antigenic

<u>ATCGCCCCCGGCCAGATGCGCGAGCCCCCGCGGCAGCATCGCCGGCACCACCAGCACC</u>

726

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polypeptides, useful as immunogenic compositions or vaccines for generating humoral or cellular immune responses against HIV in a subject, especially humans.
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Example 1; 262pp; English.

The invention describes a synthetic polynucleotide encoding 2 or more immunogenic HIV polypeptides, where at least 2 of the polypeptides are derived from different HIV subtypes. The polynucleotide is useful for immunisation, generation of packaging cell lines, or production of HIV polypeptides. The polynucleotide and its encoded proteins are useful as immunogenic compositions or vaccines for generating humoral or cellular immune responses against HIV in a subject, or for inducing neutralising antibodies against HIV. The gene delivery vector comprising the polynucleotide is also useful for DNA immunisation of, or for generating an immune response (e.g. a humoral or cellular immune response) in, a subject such as a mammal, particularly a human. This sequence encodes a human immunodeficiency virus immunogenic peptide

Sequence 4419 BP; 980 A; 1582 C; 1371 G; 486 T; 0 u; o

Similarity

99.9%;

Score 1477.4; DB 8 Pred. No. 4.3e-185;

8

Length

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RESULT 8
ADC13240
ID ADC1
XX
AC ADC1
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DT 18-D
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DE DNA
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CW expr
KW expr
KW expr
KW Rev;
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                                                                                          expression cassette; HIV Gag; Env; Int; Nef; p15RnaseH; Pol; Tat; Prot; Rev; HIV type C; gene therapy; vaccine; immunisation; HIV; ds.
                                                                                                                                                      18-DEC-2003
                                                                                                                                                                                                   ADC13240 standard;
                                                                      Human immunodeficiency virus
 05-JUL-2002; 2002WO-US021420
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The invention relates to a novel expression cassette comprising a polynucleotide sequence encoding a polypeptide including an HIV Gag, Int, Nef, p15RnaseH, Pol, Tat, Prot, or Rev polypeptide. The novel expression cassette can be used to treat HIV type C by gene therapy used in the development of a vaccine. The gene delivery vector is administered intramuscularly, intramucosally, intranasally, subcutaneously, intradermally, transdermally, intravaginally, intrarectally, orally or intravenously. The expression cassette is u for immunisation, generating packaging cell lines and producing HIV polypeptides. This polynucleotide sequence represents the DNA of an Type C related sequence of the invention.
                                                                                                                                                                                                                                                          New expression cassette comprising a polynucleotide sequence encoding polypeptide including an HIV Gag, Env, Int, Nef, p15RnaseH, Pol, Tat, Prot, or Rev polypeptide, useful for immunization, or generating packaging cell lines.
  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JUL-2001; 2001US-0303192P.
31-AUG-2001; 2001US-0316860P.
16-JAN-2002; 2002US-0349871P.
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Query Match 99.9%; Score 1477.4; DB 10; Length 4419; Best Local Similarity 99.9%; Pred. No. 4.3e-185; Matches 1478; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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                                                                                                             GCCGACAAGGGCAAAGGTGAGCCAGAACTACCCCCATCGTGCAGAACCTGCAGGGCCAGATG
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Best Local Similarity
Matches 1478; Conserv
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31-AUG-2001;
16-JAN-2002;
                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 1478; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a novel expression cassette comprising a polynucleotide sequence encoding a polypeptide including an HIV Gag, Int, Nef, p15RnaseH, Pol, Tat, Prot, or Rev polypeptide. The novel expression cassette can be used to treat HIV type C by gene therapy used in the development of a vaccine. The gene delivery vector is administered intramuscularly, intramucosally, intransablly, subcutaneously, intradermally, transdermally, intravaginally, intrarectally, orally or intravenously. The expression cassette is u for immunisation, generating packaging cell lines and producing HIV polypeptides. This polynucleotide sequence represents the DNA of an Type C related sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New expression cassette comprising a polynucleotide sequence encopolypeptide including an HIV Gag, Env, Int, Nef, p15RnaseH, Pol, Prot, or Rev polypeptide, useful for immunization, or generating packaging cell lines.
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PR 16-JA
PR 16-J Immunogenic HIV polypeptide; human immunodeficiency virus; HIV; vaccine; gene therapy; packaging cell line; humoral immune response; cellular immune response; gene delivery vector; DNA immunisation; ds. Synthetic DNA ecoding immunogenic HIV peptide #5 22-MAY-2003 ACA03522; (first entry)

05-JUL-2001; 31-AUG-2001; 16-JAN-2002; 16-JAN-2002; 05-JUL-2002; 16-JAN-2002; 16-JAN-2003. (CHIR ) CHIRON Ç 2001US-0303192P. 2001US-0316860P. 2002US-0349728P. 2002US-0349793P. 2002US-0349871P 2002WO-US021421 Barnett CORP. ws, Lian ۲;

New synthetic polynucleotides encoding antigenic HIV type B and/or type C polypeptides, useful as immunogenic compositions or vaccines for generating humoral or cellular immune responses against HIV in a subject, especially humans.

Ω

2003-221602/21.

Example 1; Fig 10; 262pp; English.

The invention describes a synthetic polynucleotide encoding 2 or more immunogenic HIV polypeptides, where at least 2 of the polypeptides are derived from different HIV subtypes. The polynucleotide is useful for immunisation, generation of packaging cell lines, or production of HIV polypeptides. The polynucleotide and its encoded proteins are useful as immunogenic compositions or vaccines for generating humoral or cellular immune responses against HIV in a subject, or for inducing neutralising antibodies against HIV. The gene delivery vector comprising the polynucleotide is also useful for DNA immunisation of, or for generating an immune response (e.g. a humoral or cellular immune response) in, a subject such as a mammal, particularly a human. This sequence encodes a human immunodeficiency virus immunogenic peptide

Sequence 4716 BP; 1041 A; 1684 C; 1463 <u>ი</u> 528 T; 0 Ų. 0 Other;

Query Match

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Score 1477.4; ₽B 8 Length 4716;

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                                                             New expression cassette comprising a polynucleotide sequence polypeptide including an HIV Gag, Env, Int, Nef, p15RnaseH, P Prot, or Rev polypeptide, useful for immunization, or generat packaging cell lines.
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31-AUG-2001; 2001US-0316860P.
16-JAN-2002; 2002US-0349871P.
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                                        Disclosure; Fig 14; 301pp; English.
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The invention relates to a novel expression cassette comprising a polynucleotide sequence encoding a polypeptide including an HIV Gag, Int, Nef, p15RnaseH, Pol, Tat, Prot, or Rev polypeptide. The novel

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                                   AAGCGGTGGATCATCCTGGGCCTGAACAAGATCGTGCGGATGTACAGCCCCGTGAGCATC
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                                                                                                                                                                                                                                                                            Immunogenic HIV polypeptide; human immunodeficiency virus; HIV; vaccine; gene therapy; packaging cell line; humoral immune response; cellular immune response; gene delivery vector; DNA immunisation; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention describes a synthetic polynucleotide encoding 2 or more immunogenic HIV polypeptides, where at least 2 of the polypeptides are derived from different HIV subtypes. The polynucleotide is useful for immunisation, generation of packaging cell lines, or production of HIV polypeptides. The polynucleotide and its encoded proteins are useful as immunogenic compositions or vaccines for generating humoral or cellular immune responses against HIV in a subject, or for inducing neutralising antibodies against HIV. The gene delivery vector comprising the polynucleotide is also useful for DNA immunisation of, or for generating an immune response (e.g. a humoral or cellular immune response) in, a subject such as a mammal, particularly a human. This sequence encodes a human immunodeficiency virus immunogenic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New synthetic polynucleotides encoding antigenic HIV type B and/or type C polypeptides, useful as immunogenic compositions or vaccines for generating humoral or cellular immune responses against HIV in a subject, especially humans.
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          GACACCATCAACGAGGAGGCCGCCGAGTGGGACCGCGTGCACCCCGTGCACGCCGGCCCC
                                                          GACCTGAACACGATGTTGAACACCGTGGGCGGCCACCAGGCCGCCATGCAGATGCTGAAG
                                                                                                                GCCTTCAGCCCCGAGGTGATCCCCCATGTTCACCGCCCTGAGCGAGGGGCGCCACCCCCCAG
                                                                                                                                                        GTGCACCAGGCCATCAGCCCCCGCACCCTGAACGCCTGGGTGAAGGTGATCGAGGAGAAG
                                                                                                                                                                        GTGCACCAGGCCATCAGCCCCCGCACCCTGAACGCCTGGGTGAAGGTGATCGAGGAGAAG
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18-DEC-2003

(first entry)

expression Rev; HIV ty on cassette; type C; gene tte; HIV Gag; Env; Int; Nef; p15RnaseH;
gene therapy; vaccine; immunisation; H; Pol; Tat;

Human immunodeficiency virus

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Query Match
Best Local :
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31-AUG-2001; 2001US-0316860P
16-JAN-2002; 2002US-0349871P
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Matches 1477;
                                                                                                                                                                                                                                                                                                     The invention relates to a novel expression cassette comprising a polynucleotide sequence encoding a polypeptide including an HIV Gag, Env. Int, Nef, p15RnaseH, Pol, Tat, Prot, or Rev polypeptide. The novel expression cassette can be used to treat HIV type C by gene therapy or used in the development of a vaccine. The gene delivery vector is administered intramuscularly, intramucosally, intranasally, subcutaneously, intradermally, transdermally, intravaginally, intrarectally, orally or intravenously. The expression cassette is useful for immunisation, generating packaging cell lines and producing HIV polypeptides. This polynucleotide sequence represents the DNA of an HIV Type C related sequence of the invention.
                                                                                                                                                                                                                                                                                   Sequence
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31-AUG-2001; 2001US-0316860P.
16-JAN-2002; 2002US-0349871P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 6; 301pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New expression cassette comprising a polynucleotide sequence encoding polypeptide including an HIV Gag, Env, Int, Nef, p15RnaseH, Pol, Tat, Prot, or Rev polypeptide, useful for immunization, or generating packaging cell lines.
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Rev; HIV type C; gene
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UNIV STELLENBOSCH.
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                                                                                                                                                     CTGCGCCCCGGCGGCAAGAAGTGCTACATGATGAAGCACCTGGTGTGGGCCCAGCCGCGAG
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ALIGNMENTS

## SOURCE ORGANISM ACCESSION VERSION KEYWORDS RESULT 1 CK215205/c LOCUS FEATURES COMMENT REFERENCE DEFINITION AUTHORS source Allard, F., Crosby, W.L., Danyluk, J., Eudes, F., Fr Genswein, B., Graf, R., Gulick, P., Hrycan, L.D., La Links, M.G., McCarthy, E.L., Monroy, A., Muzak, I., Penniket, C., Roach, J.L. and Sarhan, F. Functional Genomics of Abiotic Stress In Wheat a Unpublished (2003) Contact: Wm L Crosby University of Saskatchewan, Department of Computer Science 1C101 Engineering Building, 57 Campus Drive, Saskatoon, Saskatchewan, S7N 5A9, Canada Tel: 306 966 1769 Fax: 306 966 2033 Email: fgas\_ests@cs.usask.ca This sequence is the direct result of the Base calling soft Phred (default parameters). It is the raw base calls. To ai identification of the high quality insert the software Lucy (default parameters) has been run on this sequence. Lucy identification of the high quality insert the software Lucy identification of the high quality insert the software Lucy identification of the high quality insert the software Lucy identification of the high quality insert the software Lucy identification of the high quality insert the software Lucy identification of the high quality insert the software Lucy identification of the high quality insert the software Lucy identification of the high quality insert the software Lucy identification of the software Lucy ide FGAS027158 Triticum aestivum aestivum cDNA, mRNA sequence. CK215205 Bioinformatics Triticum aestivum CK215205.1 GI:39621309 Triticum aestivum (bread wheat) region [13,662]. te: L6B016 row: K column: Location/Qualifiers /organism="Triticum aestivum" /mol\_type="mRNA" /db\_xref="taxon:4565" /clone\_lib="Triticum aestivum FGAS: Library 6 CAP GATE 1" /clone\_lib="Triticum aestivum FGAS: Library 6 CAP GATE 1" /note="Organ: Crown and leaf; Vector: pCMV.SPORT6; Crown (50%) and leaf (50%) tissues from wheat cultivar Norstar after short exposure times to low temperature in the light and in the dark. 12 mRNA populations were combined before constructing the library. The first 6 populations: After 7 days of growth at 20Cs from wheat cultivar Norstar after short exposure times to low temperature in the light and 746 FGAS: 15. mRNA linear EST 09-DEC-2003 Library 6 CAP GATE 1 Triticum Wheat and Canola Crops Base calling software base calls. To aid in the the software Lucy sequence. Lucy identified Frick, M., G Laroche, A., Nilson, D., Gaudet, D.,

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BQ744212 749 bp mRNA linear EST 17-JUL-2002 WHE4113_A01_A01ZS Wheat salt-stressed root cDNA library Triticum aestivum cDNA clone WHE4113_A01_A01, mRNA sequence.
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Sequences have been trimmed to remove vector sequently sequence with phred score less than 20
Seq primer: SK primer.
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AGCGAGGGCGCCACCCCCAGGACCTGAACACGATGTTGAACACCGTGGGCGGCCACCAG
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                                                                                           TTCCGCGGCAACCAGCAGAACACCGCCAAGCCCTCCGTCGACATCCAGCCCGACTGGACC
                                                                                                                                                GTGAAGGTGATCGAGGAGAAGGCCTTCAGCCCCGAGGTGATCCCCCATGTTCACCGCCCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="Full tillering"
//ab_host="E. coli SOLR"
//clone_lib="Wheat salt-stressed root cDNA library"
//clone_lib="Wheat salt-stressed root cDNA library"
//note="Vector: Lambda Uni-ZAP XR, excised phagemid
pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; Hydroponic
plants grown to full tillering stage were treated with 150
mM NaCl for either 12 hours or 7 days. Root tissues of the
plants subjected to both types of treatment were collected
separately at University of California, Davis (E. Akhunov
and K. Deal in J. Dvorak's Lab). Total RNA was prepared
separately from the two samples (12h and 7day treatments),
and equal amount of RNA was then pooled. PolyA RNA was
purified from the pooled RNA, a cDNA library was made, and
the cDNA clones were in vivo excised to give pBluescript
SK(-) phagemids in J. Dvorak's lab (E. Akhunov, J. Dvorak)
at the University of California, Davis. Colony plating,
plasmid DNA preparations and DNA sequencing were performed
in the OD Anderson lab (all other authors)."
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/cultivar="Chinese Spring"
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/tissue_type="Roots"
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1 (bases 1 to 1064)

1 (bases 1 to 1064)

Allard, F., Crosby, W.L., Danyluk, J., Eudes, F., Frick, M., Gaugenswein, B., Graf, R., Gulick, P., Hrycan, L.D., Laroche, A., Links, M.G., McCarthy, E.L., Monroy, A., Muzak, I., Nilson, D., Penniket, C., Roach, J.L. and Sarhan, F.

Functional Genomics of Abiotic Stress In Wheat and Canola Unpublished (2003)

Contact: Wm L Crosby
                                                                                                                                                                                                                                                                                                                                                                      University of Saskatchewan, De
1C101 Engineering Building, 5:
Saskatchewan, S7N 5A9, Canada
Tel: 306 966 1769
Fax: 306 966 2033
                                                                                                                                                                                                                                                                                                        Email: fgas_ests@cs.usask.ca
This sequence is the direct result of the phred (default parameters). It is the raw identification of the high quality insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.
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growth chamber for 7 days under an irradiance of 200 mmol m-2 sec-1. The temperature was maintained at 20 degrees C with a 15-hr photoperiod under a relative humidity of 70%. After this period watering of plants was stopped. Four time points were sampled during a two week period; the first after wilting was observed and the last, two weeks later, consisted of live crown and leaf tissue (leaf
                                                                                                             /organism="Triticum aestivum"
/mol_type="mRNA"
/db_xref="taxon:4565"
/clone_lib="Triticum aestivum FGAS: Library 4 Gate 8'
/clone_lib="Triticum aestivum FGAS: Library 4 Gate 8'
/note="Organ: Crown and leaf; Vector: pCMV.SPORT6;
Conditions for growth: Seeds were germinated in a
water-saturated mix (50% black earth and 50% ProMix)
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tissue that was yellow was not included in sampled material).First strand synthesis in this library was done in the presence of methylated dCTP thereby protecting from internal cleavage with NotI."
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Query Match
Best Local Similarity 48.4
CL968487

OBIFCC040489 Oryza sativa Express Library Oryza sativa Cultivar-group) genomic, genomic survey sequence.
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CL968487

DEFINITION

OSIFCC040489 Oryza sativa Express Library Oryza sativa (indica cultivar-group)

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Mangoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS

Jiao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L., Wong, G.K.S., Deng, X.W. and Wang, J.

TITLE

JOURNAL

Contact: Chen Chen

Department of Bioinformatic

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FEATURES
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Chinese Academy of Sciences, I
Tel: 86-10-80481559
Fax: 86-10-80488676
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University of Saskatchewan, Department of Computations of Campus Drive, Saskatchewan, S7N SA9, Canada
Tel: 306 966 1769
Fax: 306 966 2033
Email: fgas_ests@cs.usask.ca
This sequence is the direct result of the Base Phred (default parameters). It is the raw base identification of the high quality insert the insert t
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after short exposure times to low temperature in the light and in the dark. 12 mRNA populations were combined before constructing the library. The first 6 populations: After 7/ days of growth at 20Cs from wheat cultivar Norstar after short exposure times to low temperature in the light and in the dark. 12 mRNA populations were combined before constructing the library. The first 6 populations: After 7 days of growth at 20, wheat plants were transferred to 4C in the light. 1cm crown sections and green leaf tissu were temperature exposure. The last 6 populations: After 7 days of growth at 20C, wheat plants were transferred to 4C in the dark. 1cm crown sections and green leaf tissu were separately harvested after 1, 3, and 6 hours of low temperature exposure. The last 6 populations: After 7 days of growth at 20C, wheat plants were transferred to 4C in the dark. 1cm crown sections and green leaf tissu were separately harvested after 1, 3, and 6 hours of low temperature exposure. First strand synthesis in this library was done in the presence of methylated dCTP thereby protecting from internal cleavage with NotI. In addition, this library used a primer for second strand synthesis that annealed to an artificial sequence (RNA oligo) added before first strand synthesis. Therefore when sequences from EST generated from this library will be masked for vector and adaptor sequences, an additional masking step will have to be included to mask this RNA oligo that is common to all clones (sequence
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Query Match Best Local Similarity Matches 346 406 583 289 604 544 484 466 424 523 364 304 643 244 703 184 763 229 664 124 287; CTGAACACGATGTTGAACACCGTGGGCCGCCACCAGGCCGCCATGCAGATGCTGAAGGAC CTCAACTACCACGAGCGCCTCATGAAGCTCGTCAAGCTCGGCCGCCTCCTCGGCTACGAC GACGAGGCCAACCACGGCACCTTCGACTTCGTCTTCGTGGACGCCGACAAGGACAACTAC CACCAGGCCATCAGCCCCGGCACCCTGAACGCCTGGGTGAAGGTGATCGAGGAGAAGGCC GACAAGGGCAAGGTGAGCCAGAACTACCCCATCGTGCAGAACCTGCAGGGCCAGATGGTG GACAAGATCGAGGAGGAGCAGAACAAGTGCCAGCAGAAGATCCAGCAGGCCGAGGCCGCC GTGGCCACCCTGTACTGCGTGCACGAGAAGATCGAGGTCCGCGACACCAAGGAGGCCCTG CTCAACATGCTGCAAGCTCATCGGCGCCAAGAAGACCATGGAGATCGGCGTCTACACC CGCCAGCTGCACCCCGCCCGCAGACCGGCGAGGAGCTGAAGAGCCTGTTCAACACC GAGATCACCGCCAACCACCCATGAAACCTGATGACGACGTCGGCGGACGAGGGCCAGTTC GAGAAGTTCGCCCTGAACCCCCGGCCTGCTGGAGACCAGCGAGGGCTGCAAGCAGATCATC GTCGAGATCTGCCAGCTCCCCGTCGGCGACGGCATCACCCTCTGCCGCCGCCGCA 175 TTCAGCCCCGAGGTGATCCCCATGTTCACCGCCCTGAGCGAGGGCGCCACCCCCAGGAC CACAAGATCGACTTCCGCGAGGG----CCCCGGCGCTGCCGGTGCTGGACGCGCTGCTGGAG GACATCAACCGCGAGAACTACGAGCTGGGGGCTGCCGTGCATCGAGAAGGCCGGCGTGGCG GGCTACTCCTCCTCGCCACCGCGCTCGCCATCCCCGACGACGGCACCATCTTGGCCATG GCCCCCGGCCAGATGCGCGAGCCCCGCGGCAGCACCATCGCCGGCACCACCAGCA 718 ACCATCAACGAGGAGGCCGCCGAGTGGGACCCCGTGCACCCCGTGCACGCCCCATC ATCCGCTCCTACCGCGACTTCGTCCTCGACCTCAACAAGGCCCTCGCCGACCAGCGC Conservative 5.4%; 48.2%; 0; Score 79.8; DB 7; Pred. No. 0.00015; 0; Mismatches 302; Length 1126; Indels 6 303 663 290 603 347 543 407 483 467 423 524 363 584 644 243 704 183

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An EST database from Sorghum: acid- and alkaline-treated roots
Unpublished (2003)
Other_ESTs: RHOHI_32_C05.bl_A002
Contact: Cordonnier-Pratt MM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: mmpratt@uga.edu
Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in the Human Genome Center, University of Tokyo Institute of Medical Science; plant material and RNA prepared at Texas A & M University; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to
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RHOH1_32_C05.g1_A002 Acid- and alkaline-treated roots S bicolor cDNA clone RHOH1_32_C05_A002 5', mRNA sequence.
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The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 826)
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Seq primer: Su
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Fax: 706 583 0210
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    Conservative
                                                                                                                                                  /db_xref="taxon:4558"
/db_hxref="taxon:4558"
/clone="RHOH1 32 C05 A002"
/lab_host="DH10B-T1 phage-resistant E. coli"
/clone_lib="Acid- and alkaline-treated roots"
/note="Organ: Root; Vector: pME18S-FL3; Site_1: XhoI;
/note="Organ: Root; Vector: pME18S-FL3; Site is CACCATGTGG, 3-prime DraIII site is CACCATGTGG). XhoI excises
                                                                                                                                   the cDNA insert."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Sorghum bicolor"
/mol_type="mRNA"
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48.3%;
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                                                                                                                                                                                                                                               Arizona Genomics Institute
University of Arizona
Biological Sciences West, 44
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
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                                                                                                PCR PRimers
FORWARD: gta aaa cga cgg cca gtg
BACKWARD: gga aac agc tat gac cat g
Plate: 08 row: D column: 20
Seq primer: gta aaa cga cgg cca gtg.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CB673622 807 bp mRNA 1 OSJNEe08D20.f OSJNEe Oryza sativa (japonica clone OSJNEe08D20 5', mRNA sequence.
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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OSJNEd07C09.f OSJNEd Oryza sativa (japonica clone OSJNEd07C09 5', mRNA sequence. CB662794 CB662794.1 GI:29666519 EST. Oryza sativa (japonica cultivar-group)
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                                                                                                                                                                                                                                                                                                                        GGAGCCCTTCCGCGACTACGTGGACCGCTTCTTCAAGACCCT 905
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/clone="OSJNEe08D20"
/tissue_type="Leaf"
/tissue_type="Leaf"
/dev_stage="3 week"
/lab_host="DH10B"
/clone_lib="OSJNEe"
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/note="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2: /note="Vector: pBluescript II KS +; Site_1 = 2: /note="Vector: pBluescript II KS +; Site_2: /note="Vector: pBluescript II KS +; Site_3: /note="Vector: pBluescript II KS +; Si
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Jantasuriyarat, C., Lu, G., Gowda, M., Hatfield, J., Zhou, B., Mazus Kudrna, D., Dean, R., Soderlund, C., Wing, R. and Wang, G.
Large-scale identification of ESTs involved in the interaction between rice and Magnaporthe grisea
Unpublished (2003)
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FORWARD: gta aaa cga cgg cca gtg
BACKWARD: gga aac agc tat gac cat g
Plate: 07 row: C column: 09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: http://genome.arizona.edu
PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 520 626 3967
Fax: 520 621 9288
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University of Arizona
Biological Sciences West, 448A,
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                                                                                                      CGTGGGCGGCCACCAGGCCGCCATGCAGATGCTGAAGGACACCATCAACGAGGAGGCCGC
                                                                                                                                                                                                                CATCGGCTTCGTGTCCGACGACGTCGGCCTCGACGCCGACCGCTGCAAGGTGCTCGTCAA
                                                                                                                                                                                                                                                 CACCCTGAACGCCTGGGTGAAGGTGATCGAGGAGAAGGCCTTCAGCCCCGAGGTGATCCC
                                                                                                                                           CATCGAGCAGCAGTCGCCCGACATCGCGCAGGGGGTGCACGGCCACTTCACCAAGCGCCC
CGAGCTGATGCCCCTCAGCCACGTCCTCGCCACCAAGCTCGGCGCCCCGCCTCACCGAGGT
                                   CGAGTGGGACCGCGTGCACCCCGTGCACGCCGGCCCCATCGCCCCCGGCCAGATGCGCGA
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Location/Qualifiers
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/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="OSJNEd07C09"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="Leaf"
/dev_stage="3 week"
/lab_host="DH108"
/clone_lib="OSJNEd"
/note="Vector: pBluescript II KS +; Site_1: EcoRI;
XhoI; 24 hrs after innoculation with Rice Blast (C9)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 78;
Pred. No.
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508

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JOURNAL COMMENT
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ORGANISM
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                                                                                           Local
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                                   204 GCAGACCGGCAGCGAGGTGAAGAGCCTGTTCAACACCGTGGCCACCCTGTACTGCGT
98
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Jantasuriyarat, C., Lu, G., Gowda, M., Hatfield, J., Zhou, B., Mazur, B., Kudrna, D., Dean, R., Soderlund, C., Wing, R. and Wang, G.

Large-scale identification of ESTs involved in the interaction between rice and Magnaporthe grisea

Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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OSJNEd12P19.f OSJNEd Oryza sativa (japonica cultivar-group)

Clone OSJNEd12P19 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                         BACKWARD: gga aac agc tat gac cat
Plate: 12 row: P column: 19
Seq primer: gta aaa cga cgg cca gt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.
PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  University of Arizona
Biological Sciences West,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CB666192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arizona Genomics Institute
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                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAAGCCGGTCATCCCCGACAAGTACCTCGACGAGAAGACCAT 789
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GCAGATAGAAATGGCGGCGGAGACGTTCCTCTTCACCTCCGAGTCCGTGAACGAGGGTCA
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/lab_host="DH10B"
/clone_lib="OSJNEd"
/note="Vector: pBluescript II KS
XhoI; 24 hrs after innoculation w
                                                                                                                                                                                                                                                                                                            organism="Oryza sativa/mol_type="mRNA"
cultivar="Nipponbare"
                                                                                                                                                                                                                                                                             db_xref="taxon:39947"
/clone="OSJNEd12P19"
                                                                                                                                                                                                                                                                                                                                                                                      ocation/Qualifiers
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Pred. No. 0.000
0; Mismatches
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JOURNAL COMMENT
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AUTHORS
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85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.
PCR PRimers
                                                                                                                                                                                                                                                              1 (bases 1 to 851)
Jantasuriyarat, C., Lu, G., Gowda, M., Hatfield, J., Zhou, B., Kudrna, D., Dean, R., Soderlund, C., Wing, R. and Wang, G. Large-scale identification of ESTs involved in the interaction of the interaction
                                                                                                                                                                                                                                                                                                                                                                                              Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CB645622 851 bp mRNA 1
OSJNEb07H03.f OSJNEb Oryza sativa (japonica clone OSJNEb07H03 5', mRNA sequence.
CB645622
CB645622.1 GI:29640613
                                                                                                                                                                                      Unpublished (2003)
Contact: Rod Wing
Arizona Genomics Institute
                                                                                                                                University of Arizona
Biological Sciences W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAAGCCGGTCATCCCCGACAAGTACCTCGACGAGAAGACCAT
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                                                                                                            GGAGCCCTTCCGCGACTACGTGGACCGCTTCTTCAAGACCCT
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/note="Vector: pBluescript II KS +; Site_1: EcoF
XhoI; 24 hrs after innoculation with Rice Blast
86061)"
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/mol type="mRNA"
/cultivar="Nipponbare"
/db xref="taxon:39947"
/clone="OSJNEb07H03"
/tissue_type="Leaf"
/dev stage="3 week"
/lab_host="DH108"
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 807)
Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.
Large-scale identification of ESTs involved in the interaction
between rice and Magnaporthe grisea
Unpublished (2003)
Contact: Pod Wing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A,
85721-0088, USA
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Fax: 520 621 9288
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OSJNEe07N10.f OSJNEe Oryza sativa (japonica cultivar-group)
Clone OSJNEe07N10 5', mRNA sequence.
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GAACTACCCCATCGTGCAGAACCTGCAGGGCCAGAGGTGCACCAGGCCATCAGCCCCCG
                                                                                                                                                                                    CCCCGACAGCAAGGTGGCGTGCGAGACGTGCACCAAGACCAACATGGTGATGGTGTTCGG
                                                                                                                                                                                                                   GAACAAGTGCCAGCAGAAGATCCAGCAGGCCGAGGCCGACAAGGGCAAGGTGAGCCA 383
                                                                                                                                                                                                                                                                                       GCACGAGAAGATCGAGGTCCGCGACACCCAAGGAGGCCCCTGGACAAGATCGAGGAGGAGCA
                                                                                                                  CGAGATCACCACCAAGGCCACCGTCGACTACGAGAAGATCGTCCGCGACACCTGCCGCGG
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="OSJNEe07N10"
/tissue_type="Leaf"
/dev_stage="3 week"
/lab_host="DH10B"
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/db_xref="taxon:39947"
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/note="Vector: pBluescript II KS +; S
XhoI; 24 hrs after innoculation with
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TITLE
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AUTHORS
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                           Bioinformatics
University of Saskatchewan, Department of Computer Science 1C101 Engineering Building, 57 Campus Drive, Saskatcoon, Saskatchewan, S7N 5A9, Canada
Tel: 306 966 1769
Fax: 306 966 2033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 1138)
Allard, F., Crosby, W.L., Danyluk, J., Eudes, F., Fr Genswein, B., Graf, R., Gulick, P., Hrycan, L.D., La Links, M.G., McCarthy, E.L., Monroy, A., Muzak, I., Penniket, C., Roach, J.L. and Sarhan, F. Functional Genomics of Abiotic Stress In Wheat a Unpublished (2003)
Contact: Wm. L Crosby
                                                                                                                                                                                                                                                              Email: fgas_ests@cs.usask.ca
This sequence is the direct result of the Base calling software
Phred (default parameters). It is the raw base calls. To aid in
identification of the high quality insert the software Lucy
(default parameters) has been run on this sequence. Lucy identif
the region [8,827].
Plate: L4B008 row: F_column: 04.
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/db_xref="taxon:4565"

/clone lib="Triticum aestivum FGAS: Library 4 Gate 8"

/clone lib="Triticum aestivum FGAS: Library 4 Gate 8"

/note="Organ: Crown and leaf; Vector: pCMV.SPORT6;

Conditions for growth: Seeds were germinated in a

water-saturated mix (50% black earth and 50% ProMix) in a

growth chamber for 7 days under an irradiance of 200 mmol

m-2 sec-1. The temperature was maintained at 20 degrees C

with a 15-hr photoperiod under a relative humidity of 70%
                                                                                                                                                                                                                                              ocation/Qualifiers
                                                                                                                                                                                                 organism="Triticum aestivum"
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Laroche,A.,
L., Nilson,D.,
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Query Match
Best Local Similarity
Matches 291; Conserv
Oryza sativa (japonica cultivar-group)
M Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poac Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 812)
Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou. Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G. Large-scale identification of ESTs involved in the int between rice and Magnaporthe grisea
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EST.
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Pred. No. 0.00059;
0; Mismatches 295
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                                                                                                                                         Embryophyta; Tracheophyta; a; Poales; Poaceae;
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cultivar-group)
                                                                  Zhou, B.,
                          interaction
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REFERENCE AUTHORS

TITLE

SOURCE ORGANISM VERSION KEYWORDS

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Best Local Similarity
Matches 311; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.
PCR PRimers
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Arizona Genomics Inst
University of Arizona
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Plate: 08 row: M column:
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85721-0088, USA
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Contact: Rod Wing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCACGAGAAGATCGAGGTCCGCGACACCAAGGAGGACGCCCTGGACAAGATCGAGGAGGAGGAGCA 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCAGACCGGCAGCGAGGAGCTGAAGAGCCTGTTCAACACCGTGGCCACCCTGTACTGCGT 263
                                                                                                                                                                                                                                                                                                                                                                                                      GAACTACCCCATCGTGCAGAACCTGCAGGGCCAGATGGTGCACCAGGCCATCAGCCCCCG
GTACCTCAACGACGCCGCCCATGGTCCCCGTCCGCGTCCACCCGTCCTCATCTCCAC
                            GACCAGCAACCCCCCCATCCCCGTGGGCGACATCTACAAGCGGTGGATCATCCTGGGCCT 803
                                                                                        GCCCCGCGCCACCATCGCCGGCACCACCAGCACCTGCAGGAGCAGATCGCCTGGAT
                                                                                                                                                                                                                                                CATCGAGCAGCAGTCGCCCGACATCGCGCCAGGGGGGTGCACGGCCACTTCACCAAGCGCCCC
                                                                                                                                                                                                                                                                               CATGTTCACCGCCCTGAGCGAGGGCCCCCCCCCAGGACCTGAACACGATGTTGAACAC
                                                                                                                                                                                                                                                                                                              CATCGGCTTCGTGTCCGACGACGTCGGCCTCGACGCCGACCGCTGCAAGGTGCTCGTCAA
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                                                                                                                         CGAGCTGATGCCCCTCAGCCACGTCCTCGCCACCAAGCTCGGCGCCCCGCCTCACCGAGGT
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ilarity 44.3%;
Conservative
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/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="OSJNEf08M09"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="OSJNEf"
/note="Vector: pBluescript
XhoI; Uninfected Control"
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/dev_stage="3 week"
/lab_host="DH10B"
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Pred. No. 0.00064;
0; Mismatches 391;
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CB684834
LOCUS
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Best Local Similarity
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CB684834 832 bp mRNA linear EST U9-OSJNEf14L24.f OSJNEf Oryza sativa (japonica cultivar-group) clone OSJNEf14L24 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BACKWARD: gga aac agc tat gac cat g
Plate: 14 row: L column: 24
Seq primer: gta aaa cga cgg cca gtg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu
PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       between rice and Magnaporthe grisea
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jantasuriyarat, C., Lu, G., Gowda, M., Hatfield, J., Zl
Kudrna, D., Dean, R., Soderlund, C., Wing, R. and Wang,
Large-scale identification of ESTs involved in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FORWARD: gta aaa cga cgg cca gtg
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   GAACTACCCCATCGTGCAGAACCTGCAGGGCCAGATGGTGCACCAGGCCATCAGCCCCCG
                                         CCCCGACAGCAAGGTGGCGTGCGAGACGTGCACCAAGACCATGGTGATAGTGTTCGG
                                                                              GCACGAGAAGATCGAGGTCCGCGACACCAAGGAGGCCCTGGACAAGATCGAGGAGGAGGA
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                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Oryza sativa (
/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="OSJNEf14L24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rod Wing
                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="Leaf"
/dev_stage="3 week"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="OSJNEf"
/note="Vector: pBluescript
XhoI; Uninfected Control"
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                                                                                                                                                                                                                                                                                 391;
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                                                                                                                                                                                                                                                                                                                      832;
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                                                                                                                                                                                                                                                                                                                                                              TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
                                                         source
                                                                                                                                                           Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W.,
Fenton,R.D., Oates,R. and Main,D.
Development of a genetically and physically anchored EST resource
for barley genomics: Morex unstressed seedling root cDNA library
Unpublished (2001)
TON Nov 16, 2000 this sequence version replaced gi:ll188608.
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: ruinnell
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                                                                                           Fax: 864 000 Email: rwing@clemson.edu
Total hq bases = 388
Seq primer: AATTAACCCTCACTAAAGGG
Seq primer: Requence stop: 758.
                                                                                                                                                                                                                                                                                                                                                                                                l (bases 1 to 759)
Wing,R., Close,T.J.,
Yu,Y., Henry,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BF259495

To be many linear EST 22-OCT-2001 HVSMEf0019H19f Hordeum vulgare seedling root EST library HVcDNA0007 (Etiolated and unstressed) Hordeum vulgare subsp. vulgare cDNA clone HVSMEf0019H19f, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BF259495
BF259495.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAAGCCGGTCATCCCCGACAAGTACCTCGACGAGAAGACCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTACCTCAACGACGCCGGCGCCATGGTCCCGCGTCCGCGTCCACACCGTCCTCATCTCCAC
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/organism="Hordeum vulgare
/mol_type="mRNA"
/cultivar="Morex"
                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GI:13120022
                                      subsp. vulgare"
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                               424 CACCAGGCCATCAGCCCCCGCACCCTGAACGCCTGGGTGAAGGTGATCGAGGAGAAGGCC 483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GACATCAACCGCGAGAACTACGAGCTGGGGCTGCCGTGCATCGAGAAGGCCCGGCGTGGCG
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ACCATCAACGAGGAGGCCGCCGAGTGGGACCGCGTGCACCCCGTGCACGCCGGCCCCATC
                                                                                 --- AACACCCTCTGGAACGGCTCCGTCGTGCTCCCCGCCGACGCCCCATGCGCAAGTAC
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ilarity 47.7%;
Conservative
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/note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1; Seeds were surface sterilized then germinated under axenic conditions in the dark at room temperature on filter paper with water, nystatin and cefotaxime in covered crystallization dishes. Five-day old seedling roots were then harvested, total RNA was prepared, poly(A) RNA was purified, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids. These steps were performed in the TJ Close laboratory at the University Genomics Institute (CUGI) (Regum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
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/lab_host="TJC121"
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/db_xref="taxon:112509"
/clone="HVSMEf0019H19f"
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Pred. No. 0.00069;
0; Mismatches 305; Indels
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547 GTNGAGATCTGCCAGCTCCCCGTCGGCGACGGCATCACCCTCTGCCGCCGCGCCA 601	664 GCCCCGGCCAGATGCGCGAGCCCCGCCGCCAGCATCGCCGGCACCACCAGCA 718

Search completed: March 13, Job time: 5214.18 secs 2005, 00:13:44

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Maximum DB
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Maximum Match 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Title:
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     1197.8
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APPLICANT: SRIVASTAVA, Indresh
APPLICANT: SRIVASTAVA, Indresh
APPLICANT: LIAN, Ying
APPLICANT: LIAN, Ying
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APPLICANT: HARTOG, Karin
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APPLICANT: SELBY, Hong
APPLICANT: SELBY, Mark
APPLICANT: SELBY, Mark
APPLICANT: WALKER, Christopher
TITLE OF INVENTION: IMPROVED EXPRESSION OF HIV POLYPEPTIDES AND PRODUCTION
TITLE OF INVENTION: IMPROVED EXPRESSION OF HIV POLYPEPTIDES AND PRODUCTION
TITLE OF INVENTION NUMBER: US/09/475,515A
CURRENT APPLICATION NUMBER: US/09/475,515A
CURRENT FILING DATE: 1999-12-30
NUMBER OF SEQ ID NO 75
LENGTH: 4472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: gp160.modUS4.delV1/V2.gag.modSF2 US-09-475-515-75
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Best Local Similarity
Matches 1347; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 75, Application US/09475515A Patent No. 6602705 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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                                                                                    ACCGTGGCCACCCTGTACTGCGTGCACGAGAAGATCGAGGTCCGCGACACCCAAGGAGGCC
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 CTGGAGAAGATCGAGGAGGAGCAGAACAAGTCCAAGAAGAAGGCCCAGCAGGCCGCCGCC
                                                                  ACCGTGGCCACCCTGTACTGCGTGCACCAGCGCATCGACGTCAAGGACACCAAGGAGGCC
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                                        CCCGCCGAGAGCTTCCGCTTC-----GAGGAGACCACCCCCGGCCAGAAGCAGGAG--- 1413
                                                                                                     CCCAGCCACAAGGGCCGCCCCGGCAACTTCCTGCAGAGCCGCCCCCGAGCCCACCGCCCCC
                                                                                                                                                                                        GAGGGCCACCAGATGAAGGACTGCACCGAGCGCCAGGCCAACTTCCTGGGCAAGATCTGG
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Sequence 76, Application US/09475515A

Patent NO. 6602705

GENERAL INFORMATION:
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APPLICANT: LIAN, Ying
APPLICANT: LIAN, Ying
APPLICANT: LIAN, Ying
APPLICANT: LIO, Hong
APPLICANT: SELBY, Mark
APPLICANT: SELBY, Mark
APPLICANT: MALKER, Christopher
TITLE OF INVENTION: IMPROVED EXPRESSION OF HIV POLYPEPTIDES AND PRODUCTION
TITLE OF INVENTION: OF VIRUS-LIKE PARTICLES
FILE REFERENCE: 1621.002
CURRENT APPLICATION NUMBER: US/09/475,515A
CURRENT APPLICATION UNBER: US
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CAGGGCCAGATGGTGCACCAGGCCATCAGCCCCCGCACCCTGAACGCCTGGGTGAAGGTG
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APPLICANT: ZUR MEGEDE, Jan
APPLICANT: SRIVASTAVA, Indresh
APPLICANT: LIAN, Ying
APPLICANT: HARTOG, Karin
APPLICANT: HARTOG, Karin
APPLICANT: SELBY, Mark
APPLICANT: SELBY, Mark
APPLICANT: SELBY, Mark
APPLICANT: SELBY, Mark
APPLICANT: WALKER, Christopher
TITLE OF INVENTION: IMPROVED EXPRESSION OF HIV POLYPEPTIDES AND PRODUCTION
TITLE OF INVENTION: OF VIRUS-LIKE PARTICLES
FILE REFERENCE: 1621.002
CURRENT APPLICATION NUMBER: US/09/475,515A
CURRENT FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 90
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 74
LENGTH: 4689
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Best Local Similarity 89.3%;
Matches 1347; Conservative
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GENERAL INFORMATION:
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                                                            ATCGAGGAGAAGGCCTTCAGCCCGAGGTGATCCCCATGTTCACCGCCCTGAGCGAGGGC
                                                                                                                    CAGGGCCAGATGGTGCACCAGGCCATCAGCCCCCGCACCCTGAACGCCTGGGTGAAGGTG
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GCCACCCCCAGGACCTGAACACGATGTTGAACACCGTGGGCGGCCACCAGGCCGCCATG
                                                                                                                                                                    GCCGCCGGCACCGGCAACAGCAGCCAGGTGAGCCAGAACTACCCCATCGTGCAGAACCTG
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Pred. No. 9.3e-177;
D; Mismatches 132;
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RESULT 5
US-09-475-515-73
; Sequence 73, Application US/09475515A
; Patent No. 6602705
; GENERAL INFORMATION:
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APPLICANT: ZUR MEGEDE, Jan
APPLICANT: SRIVASTAVA, Indresh
APPLICANT: LIAN, Ying
APPLICANT: HARTOG, Karin
APPLICANT: LIU, Hong
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APPLICANT: GREER, Catherine
APPLICANT: SELBY, Mark
APPLICANT: WALKER, Christopher
ITITLE OF INVENTION: IMPROVED EXPRESSION OF HIV POI
ITITLE OF INVENTION: OF VIRUS-LIKE PARTICLES
FILE REFERENCE: 1621.002
CURRENT APPLICATION NUMBER: US/09/475,515A
CURRENT FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 90
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: DAA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence
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Best Local Similarity 89.3%;
Matches 1347; Conservative
GCCG-----ACAAGGGCAAGGTGAGCCAGAACTACCCCATCGTGCAGAACCTG
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Pred. No. 9.3e-177;
0; Mismatches 132;
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RESULT 6
US-09-475-515-7
; Sequence 7, Application US/09475515A
; Patent No. 6602705
; GENERAL INFORMATION:
; APPLICANT: BARNETT, Susan
; APPLICANT: ZUR MEGEDE, Jan
; APPLICANT: SRIVASTAVA, Indresh
; APPLICANT: LIAN, Ying
; APPLICANT: HARTOG, Karin
; APPLICANT: LIU, Hong
; APPLICANT: GREER, Catherine
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; APPLICANT: WALKER, Christopher
; TITLE OF INVENTION: IMPROVED EXPRESSION OF HIV POLYPEPTIDES AND PROI
; TITLE OF INVENTION: OF VIRUS-LIKE PARTICLES
; FILE REFERENCE: 1621.002
; CURRENT APPLICATION NUMBER: US/09/475,515A
; CURRENT FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 7
; LENGTH: 2031
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
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Pred. No. 1.9e-176;
0; Mismatches 132;
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GENERAL INFORMATION:

APPLICANT: BARNETT, Susan

APPLICANT: ZUR MEGEDE, Jan

APPLICANT: SRIVASTAVA, Indresh

APPLICANT: LIAN, Ying

APPLICANT: LIAN, Ying

APPLICANT: HARTOG, Karin

APPLICANT: GREER, Catherine

APPLICANT: SELBY, Mark

APPLICANT: WALKER, Christopher

ITITLE OF INVENTION: IMPROVED EXPRESSION OF HIV POL

ITITLE OF INVENTION: OF VIRUS-LIKE PARTICLES

FILE REFERENCE: 1621.002

CURRENT APPLICATION NUMBER: US/09/475,515A

CURRENT FILING DATE: 1999-12-30
                                                                                                                                          RESULT 7
US-09-475-515-5
; Sequence 5, Application US/09475515A
; Patent No. 6602705
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; OTHER INFORMATION: Description of Artificial Sequence: synthetic; OTHER INFORMATION: HIV-Gag-protease US-09-475-515-5
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SOFTWARE: PatentIn Ver.
SEQ ID NO 5
LENGTH: 1853
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Best Local Similarity
Matches 1295; Conserv
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ORGANISM: Artificial
FEATURE:
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CCCGTGAGCATCCTGGACATCAAGCAGGGCCCCCAAGGAGCCCCTTCCGCGACTACGTGGAC
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Pred. No. 6.6e-164;
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Sequence 78, Application US/09475515A

Patent No. 6602705

GENERAL INFORMATION:

APPLICANT: BARNETT, Susan

APPLICANT: ZUR MEGEDE, Jan

APPLICANT: SRIVASTAVA, Indresh

APPLICANT: LIAN, Ying

APPLICANT: LIU, Hong

APPLICANT: LIU, Hong

APPLICANT: SELBY, Mark

APPLICANT: WALKER, Catherine

APPLICANT: WALKER, Christopher

TITLE OF INVENTION: IMPROVED EXPRESSION OF HIV POLYPEPTIDES AND

TITLE OF INVENTION: OF VIRUS-LIKE PARTICLES

FILE REFERENCE: 1621.002

CURRENT APPLICATION NUMBER: US/09/475,515A

CURRENT FILING DATE: 1999-12-30

NUMBER OF SEQ ID NOS: 90

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 78

LENGTH: 1865
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                                                  CGCTTCTACAAGACCCTGCGCGCTGAGCAGGCCAGGACGTGAAGAACTGGATGACC
                                                                     CGCTTCTCAAGACCCTGCGCGCCGAGCAGAGCACCCAGGAGGTGAAGAACTGGATGACC
                                                                                                          cccaccagcarccreeacarcceccaeeecccaaeeaecccrrcceeeacracereeac
                                                                                                                                   CCCGTGAGCATCCTGGACATCAAGCAGGGCCCCCAAGGAGCCCCTTCCGCGACTACGTGGAC
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Pred. No. 6.6e-164;
0; Mismatches 184;
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APPLICANT: BARNETT, SUBAN
APPLICANT: ZUR MEGEDE, Jan
APPLICANT: SRIVASTAVA, Indresh
APPLICANT: LIAN, Ying
APPLICANT: LIAN, Ying
APPLICANT: HARTOG, Karin
APPLICANT: LIU, Hong
APPLICANT: SELBY, Mark
APPLICANT: GREER, Catherine
APPLICANT: WALKER, Christopher
TITLE OF INVENTION: IMPROVED EXPRESSION OF HIV POLYPEPTIDES AND PRODUCTION
TITLE OF INVENTION: OF VIRUS-LIKE PARTICLES
FILE REFERENCE: 1621.002
CURRENT APPLICATION NUMBER: US/09/475,515A
CURRENT FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 90
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 79
LENGTH: 1865
                                                                                   ; LENGTH: 1865
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
US-09-475-515-79
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US-09-475-515-79
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                            Query Match
Best Local Similarity
Matches 1295; Conserv
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                           75.4%; Score 1114.6; DB 4; ilarity 85.8%; Pred. No. 6.6e-164; Conservative 0; Mismatches 184;
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                                                                                                                                 GACACCCTGCTGGTGCAGAACGCCAACCCCGACTGCAAGACCATCCTGCGCGCTCTCGGC 1008
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Qy       61 CTGCGCCCCGGCGCAAGAAGTGCTACATGATGAAGCACCTGGTGTGGGCCAGCCGCGAG	Qy 1 ATGGGCGCCCGCGCAGCATCCTGCGCGGCAAGCTGGACGCCTGGGAGCGCATCCGC	Query Match 75.4%; Score 1114.6; DB 4; Length 4319; Best Local Similarity 85.8%; Pred. No. 6.6e-164; Matches 1295; Conservative 0; Mismatches 184; Indels 30; Gaps	FEATURE: OTHER INFORMATION: De OTHER INFORMATION: HI -09-475-515-6	SEQ ID NO 6 LENGTH: 4 TYPE: DNA ORGANISM:	CURRENT APPLICATION NUMBER: US/09/475,515A ; CURRENT FILING DATE: 1999-12-30 ; NUMBER OF SEQ ID NOS: 90 ; SOFTWARE: Patentin Ver. 2.0	APPLICANT: WALKER, TITLE OF INVENTION TITLE OF INVENTION TITLE OF INVENTION	APPLICANT: HARTOO APPLICANT: LIU, I APPLICANT: GREER APPLICANT: SELEY	; APPLICANT: BARNETT, Susan ; APPLICANT: ZUR MEGEDE, Jan ; APPLICANT: SRIVASTAVA, Indresh ; APPLICANT: LIAN. Ying	US-09-475-515-6  VS-09-475-515-6  VS-09-475-515-6  VS-09-475-515-6  VS-09-475-515-A  VS-09-475-A   Q 1117	1471	QY 1414AGCAAGGACCGCGAGACCCTGACCAGCCTGAAGAGCCTGTTCGGCAACGACCCCCTG	QY 1363 CCCGCCGAGAGCTTCCGCTTCGAGGAGACCACCCCCGGCCAGAAGCAGGAG Db 1393 CCAGAAGAGCTTCAGGTTTGGGGAAGAAAAAAAACTCCCTCTCAGAAGCAGGAGCCG	1333 C	Db 1273 GAAGGACACCAAATGAAAGATTGCACTGAGAGACAGGCCAACTCAGGGAAGATCTGG  OY 1303 CCCAGCCACAAGGGCCGCCCCGGCAACTTCCTGCAGAGCCCCCCCAGCCCACCGCCCCC	1243	QY 1183 GGCCACATCGCCGCAACTGCCGCGCGCCCCCCGCAAGAAGGGGCTGCTGGAAGTGCGGCAAGAAGAAGGGCTGCTGGAAGTGCCGCCAAGAAGAAGGGCTGCTGGCGGCCGCCGCAAGAAGAAGGGCTGCTGGCGGCCGCCGCCAAGAAGAAGGGCTGCTGGCGGCCGCCGCGCAAGAAGAAGGGGCTGCTGGCGGCCGCCGCGCAAGAAGAAGGGGCTGCTGGCGGCCGCCGCGCAAGAAGAAGGGCTGCTGGCGGCCGCCGCGCAAGAAGAAGGGGCTGCTGGCGGCCGCCGCGCAAGAAGAAGGGGCTGCTGGCGGCCGCCGCGCAAGAAGAAGAAGGGCTGCTGCGGCCGCCGCGCAAGAAGAAGAAGGGCTGCTGCGGCCGCCGCGCAAGAAGAAGAAGGGGCTGCTGCGGCCGCCGCGCAAGAAGAAGAAGGGCTGCTGCGGCCGCCGCGCAAGAAGAAGAAGGGGCTGCTGCGGCCGCCGCGCAAGAAGAAGAAGAAGAAGAAGAAGAAG	1153	Db 1093 AAGGCCCGCGTGCTGGCCGAGGCGATGAGCCAGGTGACGAACCCGGCGACCATCATGATG  Qy 1123 CAGAAGAGCAACTTCAAGGGCCCCCGGCGCATCGTCAAGTGCTTCAACTGCGGCAAGGAG	
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Qy	FEATURE: OTHER INFORMATION: Description of the common response of th	CURRENT APPLICATION NUMBER: US/09/475,515A  CURRENT FILING DATE: 1999-12-30  NUMBER OF SEQ ID NOS: 90  SOFTWARE: Patentin Ver. 2.0  SEQ ID NO 9  LENGTH: 1268  TYPE: DUA  ORGANISM: Artificial Sequence	APPLICANT: HARTOG, Karin APPLICANT: LIU, Hong APPLICANT: GREER, Catherine APPLICANT: SELBY, Mark APPLICANT: WALKER, Christopher TITLE OF INVENTION: IMPROVED EXPRESSION OF HIV POLYPEPTIDES AND PRODUCTION TITLE OF INVENTION: OF VIRUS-LIKE PARTICLES FILE REFERENCE: 1621 002	t co	3	Db 1447 ATAGACAAGGAACTGTATCCTTTAACTTCCCTCAGATCACTCTTTGGCAACGACCCCTCG 1506  OY 1471 AGCCAGTAA 1479	1387 1414	QY 1303 CCCAGCCACAAGGGCCGCCCCGGCAACTTCCTGCAGAGCCGCCCCGAGCCCACCCCCCC 1362	GAGGGCCACCAGATGAAGGACTGCACCGAGCCCAGGCCAACTTCCTGGGCAAGATCTGG 130	Db 1207 GGCCACACCGCCAGGAACTGCCGCGCCCCCCCCAAGAAGGGCTGCTGGCGCCGCCCCCCCC
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GENERAL INFURFACIONE

APPLICANT: Emini, Emilio A.

APPLICANT: Youil, Rima

APPLICANT: Youil, Rima

APPLICANT: Sett, Andrew J.

APPLICANT: Chen, Ling

APPLICANT: Kaslow, David C.

APPLICANT: Kaslow, David C.

APPLICANT: Shiver, John W.

APPLICANT: Toner, Timothy J.

APPLICANT: Cosimito, Danilo R.

TITLE OF INVENTION: ENHANCED FIRST GENERATION ADENOVIRUS

TITLE OF INVENTION: VACCINES EXPRESSING CODON OPTIMIZED HIV1-GAG, POL,

TITLE OF INVENTION UNDER: US/09/952,060

CURRENT APPLICATION NUMBER: US/09/952,060

CURRENT APPLICATION NUMBER: US/09/952,060

CURRENT APPLICATION NUMBER: 60/317,814

PRIOR APPLICATION NUMBER: 60/317,814

PRIOR APPLICATION NUMBER: 60/279,056

PRIOR FILING DATE: 2001-09-07

PRIOR APPLICATION NUMBER: 60/279,056

PRIOR FILING DATE: 2001-03-27

PRIOR APPLICATION NUMBER: 60/233,180

PRIOR FILING DATE: 2001-09-15

NUMBER OF SEQ ID NOS: 38

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 27

LENGTH: 1521

TYPE: DNA
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Codon optimized
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Best Local Similarity 80.3
Matches 1205; Conservative
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APPLICANT: Shiver, John W.
Davies, Mary Ellen
Freed, Daniel C.
Liu, Margaret A.
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                                                                                                                                                                                                                                                                                                        ; SEQUENCE DESCRIPTION: US-09-974-702-1
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US-09-974-702-1
                                                                                                                                                                                                                                       Matches 1205;
                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                  TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1532 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: both
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US/09/974,702
FILING DATE: 09-Oct-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/017,981
FILING DATE: 03-FEB-1998
APPLICATION NUMBER: US60/037,854
FILING DATE: 07-FEB-1997
APPLICATION NUMBER: GB9705040.5
FILING DATE: 12-MAR-1997
APPLICATION NUMBER: 36,545
FILING DATE: 12-MAR-1997
APPLICATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 19730
TELECOMMUNICATION INFORMATION:
TELECHONE: 732-594-4720
TELEFAX: 732-594-4720
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OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000, 126 E. Lincoln Ave.
CITY: Rahway
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MEDIUM TYPE: Diskette
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TITLE OF INVENTION: Synthetic HIV
NUMBER OF SEQUENCES: 1
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                                   COUNTRY: USA
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Pred. No. 1.4e-142;
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CURRENT APPLICATION NUMBER: US/09/818,443
CURRENT FILING DATE: 2001-09-13
PRIOR APPLICATION NUMBER: PCT/US00/18332
PRIOR FILING DATE: 2000-07-03
PRIOR APPLICATION NUMBER: 60/148,981
PRIOR FILING DATE: 1999-08-13
PRIOR APPLICATION NUMBER: 60/142,631
PRIOR APPLICATION NUMBER: 60/142,631
PRIOR FILING DATE: 1999-07-06
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1532
TYPE: DNA
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APPLICANT: Chen, Ling

APPLICANT: Shiver, John W.

APPLICANT: Bett, Andrew J.

APPLICANT: Casimiro, Danilo R.

APPLICANT: Caulfield, Michael J.

APPLICANT: Chastain, Michael A.

APPLICANT: Emini, Emilio A.

TITLE OF INVENTION: ADENOVIRUS CARRYING GAG GE

FILE REFERENCE: 20440YIA
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; OTHER INFORMATION: Optimized human HIV-1 US-09-818-443-1
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Best Local Similarity
Matches 1205; Conserv
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241 ACCGTGGCCACCCTGTACTGCGTGCACGAGAAGATCGAGGTCCGCGACACCAAGGAGGCC 30	QY 181 ATCCGCCAGCTGCACCCCCCCCCCCGCAGACCCGCCAGCCA	QY 121 CTGGAGAAGTTCGCCCTGAACCCCGGCCTGCTGGAGACCAGCGAGGCCAAGCAGATC 180	QY 61 CTGCGCCCGGCGAAGAAGTGCTACATGATGAAGCACCTGGTGTGGGCCAGCCGGAG 120	QY 1 ATGGGCGCCCAGCATCCTGCGGCGGCAAGCTGGACGCCTGGAAGCTGGAAGCTGGAAGCTGCATCCGC 60	Query Match 66.0%; Score 976.6; DB 4; Length 37474; Best Local Similarity 80.2%; Pred. No. 1.4e-142; Matches 1205; Conservative 0; Mismatches 274; Indels 24; Gaps 4;	ORGANI FEATUR OTHER S-09-952-	SOFTWARE: FastSEQ for SEQ ID NO 25 LENGTH: 37474	ECT IN NOS. 38	PRIOR FILING DATE: 2001-09-14 PRIOR FILING DATE: 2001-09-07 PRIOR FILING DATE: 2001-09-07 PRIOR FILING DATE: 2001-09-07	CURRENT FILING DATE: 2001-09-14  BELICATION NUMBER: US/09/952, CURRENT FILING DATE: 2001-09-14	APPLICANT TITLE OF TITLE OF	APPLICANT: BELC, AMDREW J.  APPLICANT: Chen, Ling  APPLICANT: Kaslow, David C  APPLICANT: Shiver, John W.	GENERAL INFORMATION: APPLICANT: Emini, Emilio APPLICANT: Youil, Rima APPLICANT: Youil, Rima	ESULT 15 S-09-952-060-25 Sequence 25, Appl	Db 1510 TAA 1512		1369 GAGAGCTTCCGCTTCGAGGAGACCACC	
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1309 CACAAGGGCCGCCCGGCAACTTCCTGCAGAGCCGCCCCGAGCCCACCGCCCCCCCC				352 AGGGTGCTGAGGGCCATGTCCCAGGTGACCAACTCCGCCACCATCATGATGCAGAGG	GGGGGCCCTGGTCACAAGGCC	955 CTGCTGCTGCAGAACGCCAACCCCGACTGCAAGACCATCCTGCGCGCTCTO	895 TTCAAGACCCTGCGCGCGAGCAGAGCACCCAGGAGGTGAAGAACTGGATGACCGACACC 954	GCTTC	775 ATCTACAAGCGGTGGATCATCCTGGGCCTGAACAAGATCGTGCGGATGTACAGCCCCGTG 834	715 AGCACCCTGCAGGAGCAGATCGCCTGGATGACCAGCAACCCCCCATCCCCGTGGGCGAC 774	655 GGCCCATCGCCCCGGCCAGATGCGCGAGCCCCGCGGCAGCACATCGCCGGCACCACC 714	595 CTGAAGGACACCATCAACGAGGAGGCCGCCGAGTGGGACCGCGTGCACCCCGTGCACGCC 654	535 CCCCAGGACCTGAACACGATGTTGAACACCGTGGGCGGCCACCAGGCCGCCATGCAGATG 594	475 GAGAAGGCCTTCAGCCCCGAGGTGATCCCCATGTTCACCGCCCTGAGCGAGGGGGCCCACC 534	415 CAGATGGTGCACCAGGCCATCAGCCCCCGCACCCCTGAACGCCTGGGTGAAGGTGATCGAG 474	359CCGCCGACAAGGGCAAGGTGAGCCAGAACTACCCCATCGTGCAGAACCTGCAGGGC 414	301 CTGGACAAGATCGAGGAGGAGCAGAACAAGTGCCAGCAGGAGAATCCAGCAGGCCGAGG 358 	1512 ACAGTGGCTACCCTGTACTGTGCACCAGAAGATTGATGTGAAGGACACCAAGGAGGCC 1571

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2772 TAA 2774	1477 TAA 1479	2712 AAGGAGCTGTACCCCCTGGCCTCCCTGAGGTCCCTGTTTTGGCAACGACCCCTCCTCCCAG	1417 AAGGACCGCGAGACCCTGACCAGCCTGAAGAGCCTGTTCGGCAACGACCCCCTGAGCCAG	2652 GAGTCCTTCAGGTTTGGGGAGGAGAAGACCACCCCCAGCCAG	1369 GAGAGCTTCCGCTTCGAGGAGACCACCCCCGGCCAGAAGCAGGAGAGC 1416
		771	176	711	116
	2772 TAA 2774	1477 TAA 1479 	2712 AAGGAGCTGTACCCCTGGCCTCCCTGAGGTCCCTGTTTGGCAACGACCCCTCCTCCCAG 2771 1477 TAA 1479     2772 TAA 2774	1417 AAGGACCGCGAGACCCTGACCAGCCTGAAGAGCCTGTTCGGCAACGACCCCCTGAGCCAG 1476	2652 GAGTCCTTCAGGTTTGGGGAGAGACACACCCCAGAAGCAAGAGAGAG

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Title:
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Maximum Match 100%
Listing first 45 summaries
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Copyright (c) 1993 - 2005 Compugen Ltd.
/ Cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
/ cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
/ cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
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/ cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
/ cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
/ cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

110 110 110	Result No.
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100.0 100.0 99.9 99.9 99.9 99.9	% Query Match
1479 1479 3162 3462 4419 4419 4483 4606 4615 47102	% Query Match Length DB
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## ALIGNMENTS

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US-09-967-464-63
; Sequence 63, Application US/09967464
; Publication No. US20030138453A1
; GENERAL INFORMATION:
; APPLICANT: O'Hagan, Derek
; APPLICANT: O'Hagan, Derek
; APPLICANT: Dotten, Gillis
; APPLICANT: Dotten, Mamchan
; APPLICANT: Dotten
; APPLICANT: Dotten
; APPLICANT
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APPLICANT: Zur Megede, Jan
APPLICANT: Barnett, Susan W.
APPLICANT: Barnett, Susan W.
APPLICANT: Egnelbrecht, Susan
APPLICANT: Egnelbrecht, Susan
APPLICANT: van Rensburg, Estrelita Janse
TITLE OF INVENTION: POLYMUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
TITLE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF
FILE REFERENCE: PP01631.102
CURRENT APPLICATION NUMBER: US/09/899,575
CURRENT FILING DATE: 2001-07-05
PRIOR APPLICATION NUMBER: 09/475,704
PRIOR FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 135
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 1479
TYPE: NAM
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Publication No. US20030223961A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                   Query Match 100.0%;
Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                     Matches 1479;
                                                                                                                                                                                                                                                                                                                                  FEATURE:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1479
TYPE: DNA
ORGANISM: Artificial Sequence
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Pred. No. 4.1e-308;
Mismatches 0;
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Sequence 18, Application US/10190435

Publication No. US20030143248A1

Publication No. US20030143248A1

Publicant: DARMATION:
APPLICANT: ZUR MEGEDE, Jan
APPLICANT: LIAN, Ying
APPLICANT: LIAN, Ying
APPLICANT: WAN RENSBURG, Estrelita J.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, AND USES THEREOF
FILE REFERENCE: PP18133.003 / 2302-18133
CURRENT APPLICATION NUMBER: US/10/190,435
CURRENT FILING DATE: 2002-12-30
NUMBER OF SEQ ID NOS: 319
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 18
LENGTH: 3162
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: GagRTmut_C
US-10-190-435-18
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Best Local Similarity 99.9%;
Matches 1478; Conservative
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                                                                                                                              CTGGACAAGATCGAGGAGGAGCAGAACAAGTGCCAGCAGAAGATCCAGCAGGCCGAGGCC
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Pred. No. 8.8e-308;
0; Mismatches 1;
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RESULT 4 US-10-190-435-16 ; Sequence 16, Application US/10190435

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; Publication No. US20030143248A1
; GENERAL INFORMATION:
; APPLICANT: ZUR MEGEDE, Jan
; APPLICANT: BARNETT, Susan W.
; APPLICANT: BARNETT, Susan W.
; APPLICANT: ENGELBRECHT, Susan
; APPLICANT: VAN RENSBURG, Estrelita J.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: PP18133.003 / 2302-18133
; CURRENT APPLICATION NUMBER: US/10/190,435
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 319
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 16
; LENGTH: 3462
; TYPE: DNA
ORGANISM: Artificial Sequence
; FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: GagProtInaR7
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Best Local Similarity 99.9%;
Matches 1478; Conservative
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                GACCTGAACACGATGTTGAACACCGTGGGCGGCCACCAGGCCGCCATGCAGATGCTGAAG
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Pred. No. 8.8e-308;
0; Mismatches 1; I
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RESULT 5
US-10-190-435-19

US-10-190-435-19
; Sequence 19, Application US/10190435
; Publication No. US20030143248A1
; GENERAL INFORMATION:
; APPLICANT: ZUR MEGEDE, Jan
; APPLICANT: BARNETT, Susan W.
; APPLICANT: LIAN, Ying
; APPLICANT: LIAN, Ying
; APPLICANT: VAN RENSBURG, Estrelita J.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE
TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES AND USES THEREC
; FILE REFERENCE: PP18133.003 / 2302-18133
; CURRENT APPLICATION NUMBER: US/10/190,435
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 319
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 19
; LENGTH: 4419
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                                                  CTGGACATCAAGCAGGGCCCCAAGGAGCCCTTCCGCGACTACGTGGACCGCTTCTTCAAG
                                                                    CTGGACATCAAGCAGGGCCCCAAGGAGCCCTTCCGCGACTACGTGGACCGCTTCTTCAAG
                                                                                                             AAGCGGTGGATCATCCTGGGCCTGAACAAGATCGTGCGGATGTACAGCCCCCGTGAGCATC
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420 366 360 306 300 246 240 186 180

426

960 966

906 900

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999 660 909 600 546 540 486 480

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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description
US-10-190-435-19
                                                                                           ATGGGCGCCCGCGCCAGCATCCTGCGCGCGGCGAAGCTGGAACGCCTGGGAGCGCATCCGC
CTGCGCCCCGGCGAAGAAGTGCTACATGATGAAGCACCTGGTGTGGGCCAGCCGCGAG
                       CTGCGCCCCGGCGGCAAGAAGTGCTACATGATGAAGCACCTGGTGTGGGCCCAGCCGCGAG
                                                                      ATGGGCGCCCGCGCATCCTGCGCGCGGCGAAGCTGGACGCCTGGGAGCGCATCCGC
                                                                                                                                                           99.98;
                                                                                                                                                                                                                                  Description of Artificial Sequence: GagRTmutTatRevNef_C
                                                                                                                                           0;
                                                                                                                                           Score 1477.4; DB 15;
Pred. No. 8.7e-308;
0; Mismatches 1; 1
                                                                                                                                           Indels
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61 67	1 ATGGGCGCCCGCGCAGCATCCTGCGCGGCAAGCTGGACGCCTGGGAGCGCATCC	Query M Best Lo Matches	; ORGANISM: ARTHICIAL Sequence; FEATURE: ; FEATURE: ; OTHER INFORMATION: Description of Artificial Sequence: ; OTHER INFORMATION: GagRTmutTatRevNef_C US-10-190-305A-14	OBS OBS OS	3665	; APPLICANT: BARNETT, Susan ; APPLICANT: LIAN, Ying ; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE B AND/OR ; TITLE OF INVENTION: TYPE C POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF	Sequ Publ GENI API	SULT 6 -10-190-305A-14	QY 1441 CTGAAGAGCCTGTTCGGCAACGACCCCCTGAGCCAGTAA 1479	QY 1381 TTCGAGGAGACCACCCCCGGCCAGAAGCAGGAGAGCAAGGACCGCGAGACCCTGACCAGC	QY 1321 CCCGGCAACTTCCTGCAGAGCCGCCCGAGCCCCACCGCCCCCCCC	Qy 1261 GACTGCACCGAGCGCCAGGCCAACTTCCTGGGCAAGATCTGGCCCAGCCACAAGGGCCGC	QY 1201 TGCCGCGCCCCCCGCAAGAAGGGCTGCTGGAAGTGCGGCAAGGAGGGCCCACCAGATGAAG	QY 1141 GGCCCCCGGCGATCGTCAAGTGCTTCAACTGCGGCAAGGAGGGCCACATCGCCCGCAAC	QY 1081 CTGGCCGAGGCGATGAGCCAGGCCAACACCAGCGTGATGATGCAGAAGAGCAACTTCAAG	QY 1021 CTGGAGGAGATGATGACCGCCTGCCAGGGGTGGGCGGGCCCCAGCCACAAGGCCCGCGTG	QY 961 GTGCAGAACGCCAACCCCGACTGCAAGACCATCCTGCGCGCGC
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1141 GGCCCCGGCGCATCGTCAAGIGCTTCAACTGCGGCAAGGAGGGCCACATCGCCGCAAC 1200	081 CTGGCCGAGGCGATGAGCCAGGCCAACACCAGCGTGATGATGCAGAAGAGCAAC	021 CTGGAGGAGATGATGACCGCCTGCCAGGGCGTGGGCGCCCAGCCCAGCCACCACCACCGCGTGGCGCGCGC	961 GTGCAGAACGCCAACCCCGACTGCAAGACCATCCTGCGCGCGC	901 ACCCTGCGCGCCGAGCAGAGCACCCAGGAGGTGAAGAACTGGATGACCGACACCCCTGCTG 960	841 CTGGACATCAAGCAGGGCCCCAAGGAGCCCTTCCGCGACTACGTGGACCGCTTCTTCAAG 900	781 AAGCGGTGGATCATCCTGGGCCTGAACAAGATCGTGCGGATGTACAGCCCCGTGAGCATC 840	721 CTGCAGGAGCAGATCGCCTGGATGACCAGCAACCCCCCCATCCCCGTGGGCGACATCTAC 780	661 ATCGCCCCCGGCCAGATGCGCGAGCCCCGCGGCAGCACCAGCACCCAGCACC 720	601 GACACCATCAACGAGGAGGCCGCCGAGTGGGACCGCGTGCACCCCGTGCACGCCGGCCCC 660	541 GACCTGAACACGATGTTGAACACCGTGGGCGGCCACCAGGCCGCCATGCAGATGCTGAAG 600	81 GCCTTCAGCCCCGAGGTGATCCCCCATGTTCACCGCCCTGAGCGAGGGCGCCACCCCCCAG	421 GTGCACCAGGCCATCAGCCCCCGCACCCTGAACGCCTGGGTGAAGGTGATCGAGGAGAAG 480	361 GCCGACAAGGCAAGGTGAGCCAGAACTACCCCATCGTGCAGAACCTGCAGGGCCAGATG 420	301 CTGGACAAGATCGAGGAGGAGCAGAACAAGTGCCAGCAGAAGATCCAGCAGGCCGAGGCC 360	241 ACCGTGGCCACCCTGTACTGCGTGCACGAGAAGATCGAGGTCCGCGACACCAAGGAGGCC 300	181 ATCCGCCAGCTGCACCCCGCCCTGCAGACCGGCAGCGAGGAGCTGAAGAGCCTGTTCAAC 240	121 CTGGAGAAGTTCGCCCTGAACCCCGGCCTGCTGGAGACCAGCGAGGGCTGCAAGCAGATC 180

8	Qy db	8 8	B &	B 8	용 성	Query Ma Best Loc Matches		SE	SOF	; APP	APP APP APP	US-10- ; Sequ ; Publ	Db dd	S B	8 1	B 6	B 8	φ Q
301 CTGGACAAGATCGAGGAGGAGCAGAACAAGTGCCAGCAGAAGATCCAGCAGGCCGAGGCC 360	241 ACCGTGGCCACCCTGTACTGCGTGCACGAGAAGATCGAGGTCCGCGACACCAAGGAGGCC 300	181 ATCCGCCAGCTGCACCCCCGCCCTGCAGACCGGCAGCGAGGAGCTGAAGAGCCTGTTCAAC 240	121 CTGGAGAAGTTCGCCCTGAACCCCGGCCTGCTGGAGACCAGCGAGGGCTGCAAGCAGATC 180	61 CTGCGCCCCGGCGCAAGAAGTGCTACATGATGAAGCACCTGGTGTGGGCCAGCCGCGAG 120	1 ATGGGCGCCCGCGCCAGCATCCTGCGCGGCGCAAGCTGGACGCCTGGGAGCGCATCCGC 60	y Match 99.9%; Score 1477.4; DB 15; Length 4483; Local Similarity 99.9%; Pred. No. 8.7e-308; hes 1478; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	RMATION: Descripti RMATION: gp160mod. 35	Q ID NO 35 LENGTH: 4483 TYPE: DNA ORGANISM: Artificial Sequence	CURRENT APPLICATION NUMBER: US/10/190,435 CURRENT FILING DATE: 2002-12-30 NUMBER OF SEQ ID NOS: 319 SOFTWARE: Patentin Ver. 2.0	LICANT: VAN RENSBURG, ESTRELITA J.  LE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C  LE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF  R REFERENCE: PP18133.003 / 2302-18133	LICANT: ZUR MEGEDE, Jan LICANT: BARNETT, Susan W. LICANT: LIAN, Ying LICANT: ENGELBRECHT. Susan	US-10-190-435-35 ; Sequence 35, Application US/10190435 ; Publication No. US20030143248A1 ; GENERAL INFORMATION:	1447 CTGAAGAGCCTGTTCGGCAACGACCCCCTGAGCCAGAAA 1485	1387 TTCGAGGAGACCCCCCGGCCAGAAGCAGGAGGCAAGGACCGCGAGACCCTGACCAĞC 1446 1441 CTGAAGAGCCTGTTCGGCAACGACCCCCTGAGCCAGTAA 1479	381 TTCGAGGAGACCACCCCCGGCCAGAAGCAGGAGGAGGAAGGACCGGGAGACCCTGACCAGC 14	1321   CCCGGCAACTTCCTGCAGAGCCGCCCCGAGCCCAGCCGCCCCCCCC	1261 GACTGCACCGAGCCCAGGCCAACTTCCTGGGCAAGATCTGGCCCAGCCACAAAGGGCCGC 1320	1201 TGCCGCGCCCCCCGCAAGAAGGGCTGCTGGAAGTGCGGCAAGGAGGGCCACCAGATGAAG 1260 
4d 8	dg dg	B &	? B &	d dd A	B &	Db Qy	db Qy	Qy db	dg VQ	B 8	. B &	Qy Db	Qy Db	영 영	Db 43	§ B	<b>&amp;</b> &	Db Qy
1381 TTCGAGGAGACCACCCCCGGCCAGAAGCAGGAGGACCAGAGGACCCGAGAGCCAGC 1440	21 CCCGGCAACTTCCTGCAGAGCCGCCCCGAGAGCCCACCGCCCCCCCC	261 GACTGCACCGAGCGCCAGGCCAACTTCCTGGGCAAGATCTGGCCCAGCCACAAGGGCCGCGCGCG	TIGUEGE COCCECAGAGAGGETTGCTGGAAGTGCGGCAAGGAGGGCCACCAGATGAAGTGCGCAAGGAGGAGGCCACCAGATGAAGTGCGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	.141 GGCCCCCGGCGCATCGTCAAGTGCTTCAACTGCGGCAAGGAGGGCCACATCGCCCGCAAC	081 CTGGCCGAGGCGATGAGCCAGGCCAACACCAGCGTGATGATGCAGAAGAGAGCAACTTCAAG	021 CTGGAGAGATGATGACCGCCTGCCAGGGCGTGGGCGGCCCCAGCCACAAGGCCCGCGTG	961 GTGCAGAACGCCAACCCCGACTGCAAGACCATCCTGCGCGCGTCTCGGCCCCGGCGCGCAGC 1020	901 ACCCTGCGCGCGAGCAGCACCCAGGAGGTGAAGAACTGGATGACCGACACCCTGCTG 960 	841 CTGGACATCAAGCAGGGCCCCAAGGAGCCCTTCCGCGACTACGTGGACCGCTTCTTCAAG 900	781 AAGCGGTGGATCATCCTGGGCCTGAACAAGATCGTGCGGGATGTACAGCCCCGTGAGCATC 840	721 CTGCAGGAGCAGATCGCCTGGATGACCAGCAACCCCCCCATCCCCGTGGGCGACATCTAC 780	661 ATCGCCCCGGCCAGATGCGCGAGCCCCGCGGCAGCAGCGACATCGCCGGCACCACCAGCACC 720	601 GACACCATCAACGAGGAGGCCGCCGAGTGGGACCGCGTGCACCCCGTGCACGCCGGCCCC 660	541 GACCTGAACACGATGTTGAACACCGTGGGCGGCCACCAGGCCGCCATGCAGATGCTGAAG 600	## GCCTTCAGCCCCGAGGTGATCCCCCATGTTCACCGCCCTGAGCGAGGGCGCCACCCCCCAG	TGCACCAGGCCATCAGCCCCCGCACCCTGAACGCCTGGGTGAAGGTGATCGAGCCACCACCACCCTGGGTGAACGCCTGGGTGAAGGTGATCGAGGT	ĠŔĊŔĀĠĠĠĊŔĀĠĠŦĠŔĠĊĊŔĠŔŔĊŦŔĊĊĊŔŦĊĠŦĠĊŔĠŔŔĊĊŦĠĊŔĠĠĠĊĊ ĊŔĊĊŔĠĠĊĊĸŢĊŔĠĊĊĊĊĠĊŔĊĊĊŢĠŖŖĊĠĊĊŢĠĠĠŢĠĸŖĠŢĠĸŢĊĠŔĠij	3305 CTGGACAAGATCGAGGAGGAGCAGAACAAGTGCCAGCAGAAGATCCAGCAGGCCGAGGCC 3364 361 GCCGACAAGGGCAAGGTGAGCCAGAACTACCCCCATCGTGCAGAACCTGCAGGGCCAGATG 420

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RESULT 8

US-10-190-435-34

; Sequence 34, Application US/10190435
; Publication No. US20030143248A1
; GENERAL INFORMATION:
; APPLICANT: ZUR MEGEDE, Jan
; APPLICANT: LIAN, Ying
; APPLICANT: LIAN, Ying
; APPLICANT: VAN RENSBURG, Estrelita J.
; APPLICANT: VAN RENSBURG, Estrelita J.
; APPLICANT: VAN RENSBURG, Estrelita J.
; TITLE OF INVENTION: POLYMUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
TITLE OF INVENTION: POLYMPEPTIDES, POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: PP18133.003 / 2302-18133
; CURRENT APPLICATION NUMBER: US/10/190,435
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 319
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 34
; LENGTH: 4606
; TYPE: DNA
. OPGANISM: Artificial Sequence
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Best Local Similarity
Matches 1478; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence FEATURE:
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GACCTGAACACGATGTTGAACACCGTGGGCCGCCACCAGGCCGCCATGCAGATGCTGAAG
                                                       GCCTTCAGCCCCGAGGTGATCCCCCATGTTCACCGCCCTGAGCGAGGGGGCGCCACCCCCCAG
                                                                                                          GTGCACCAGGCCATCAGCCCCCGCACCCTGAACGCCTGGGTGAAGGTGATCGAGGAGAAG
                                                                                                                                GTGCACCAGGCCATCAGCCCCCGCACCCTGAACGCCTGGGTGAAGGTGATCGAGGAGAAG
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                                 GCCTTCAGCCCCGAGGTGATCCCCATGTTCACCGCCCTGAGCGAGGGGCGCCACCCCCCAG
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CTGAAGAGCCTGTTCGGCAACGACCCCCTGAGCCAATAA 4606
                    CTGAAGAGCCTGTTCGGCAACGACCCCCTGAGCCAGTAA 1479
                                                              TTCGAGGAGACCACCCCGGCCAGAAGCAGGAGAGAGCAAGGACCGCGAGACCCTGACCAGC
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RESULT 9
US-10-190-435-36
; Sequence 36, Application US/10190435
; Publication No. US20030143248A1
; GENERAL INFORMATION:
; APPLICANT: ZUR MEGEDE, Jan
; APPLICANT: BARNETT, Susan W.
; APPLICANT: LIAN, Ying
; APPLICANT: ENGELBRECHT, Susan

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; APPLICANT: VAN RENSBURG, Estrelita J.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
; TITLE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: PP18133.003 / 2302-18133
; CURRENT APPLICATION NUMBER: US/10/190,435
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 319
; SOFTWARE: PATENTIN Ver. 2.0
; SEQ ID NO 36
; LENGTH: 4615
TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
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Best Local Similarity
Matches 1478; Conserv
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Pred. No. 8.7e-308;
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RESULT 10

US-10-190-435-38

; Sequence 38, Application US/10190435
; Publication No. US20030143248A1
; GENERAL INFORMATION: Jan
; APPLICANT: ZUR MEGEDE, Jan
; APPLICANT: HAN, Ying
; APPLICANT: LIAN, Ying
; APPLICANT: ENGELBRECHT, Susan
; APPLICANT: VAN RENSBURG, Estrelita J.
; TITLE OF INVENTION: POLYMUCLEOTIDES ENCODING ANTIGENIC HIV
; TITLE OF INVENTION: POLYMUCLEOTIDES, POLYPEPTIDES, POLYPEPTIDES, NOLYPEPTIDES AND USES THE REFERENCE: PP18133.03 / 2302-18133
; CURRENT APPLICATION NUMBER: US/10/190,435
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 319
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
; LENGTH: 4702
; TYPE: DNA
; ORGANISM: Artificial Sequence
; PEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: gp160mod.TV1-gagmod.BW965
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                                                                     ACCCTGCGCGCCGAGCAGCACCCCAGGAGGTGAAGAACTGGATGACCGACACCCTGCTG
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RESULT 11

US-10-190-435-17

; Sequence 17, Application US/10190435
; Publication No. US20030143248A1
; GENERAL INFORMATION:
; APPLICANT: ZUR MEGEDE, Jan
APPLICANT: LIAN, Ying
; APPLICANT: LIAN, Ying
; APPLICANT: LIAN, Ying
; APPLICANT: VAN RENSBURG, Estrelita J.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
TITLE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: PP18133.003 / 2302-18133
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 319
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 17
; LENGTH: 4716
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER TINFORMATION: TOTAL 
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CTGGAGAAGTTCGCCCTGAACCCCGGCCTGCTGGAGACCAGCGAGGGCTGCAAGCAGATC
                                                                                                    CTGCGCCCCGGCGAAGAAGTGCTACATGATGAAGCACCTGGTGTGGGCCAGCCGCGAG
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Conservative
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Sequence 13, Application US/10190305A; Publication No. US20030198621A1; Publication No. US20030198621A1; GENERAL INFORMATION:

APPLICANT: ZUR MEGEDE, Jan
APPLICANT: LIAN, Ying
APPLICANT: LIAN, Ying
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYP)
TITLE OF INVENTION: TYPE C POLYPEPTIDES, POLYPEPTIDES AND USE;
FILE REFERENCE: 2302-18702 / 18702.002
CURRENT APPLICATION NUMBER: US/10/190,305A
CURRENT FILING DATE: 2002-07-05
NUMBER OF SEQ ID NOS: 93
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 13
LENGTH: 4716
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US-10-190-305A-13
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Best Local Similarity
Matches 1478; Conserv
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Pred. No. 8.7e-308;
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                  CTGAAGAGCCTGTTCGGCAACGACCCCCTGAGCCAGTAA 1479
                                                                                             TTCGAGGAGACCACCCCCGGCCAGAAGCAGGAGAGCAAGGAACCGCGAGACCCTGACCAGC
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CTGAAGAGCCTGTTCGGCAACGACCCCCTGAGCCAGAAA 1485
                                                                          TTCGAGGAGACCACCCCGGCCAGAAGCAGGAGAGCAAGGACCGCGAGACCCTGACCAGC
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Sequence 20, Application US/10190435
; Publication No. US20030143248A1
; GENERAL INFORMATION:
; APPLICANT: ZUR MEGEDE, Jan
APPLICANT: LIAN, Ying
; APPLICANT: LIAN, Ying
; APPLICANT: ENGELBRECHT, Susan
; APPLICANT: VAN RENSBURG, Estrelita J.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES AND USES THEREOF
FILE REFERENCE: P18133.003 / 2302-18133
; CURRENT APPLICATION NUMBER: US/10/190,435
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 319
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 20
; LENGTH: 2742
; TYPE: DNA
. OPGANISM: Artificial Semigroe
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US-10-190-435-20
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Best Local Similarity 99.9%;
Matches 1477; Conservative
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OTHER INFORMATION: Description of Artificial Sequence: GagTatRevNef_C
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GACCTGAACACGATGTTGAACACCGTGGGCGGCCACCAGGCCGCCATGCAGATGCTGAAG
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                                                                                                                                      GCCTTCAGCCCCGAGGTGATCCCCCATGTTCACCGCCCTGAGCGAGGGCGCCACCCCCCAG
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                                                    GACCTGAACACGATGTTGAACACCGTGGGCGGCCACCAGGCCGCCATGCAGATGCTGAAG
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RESULT 14
US-10-190-305A-15
; Sequence 15, Application US/10190305A
; Publication No. US20030198621A1
; GENERAL INFORMATION:
; APPLICANT: ZUR MEGEDE, Jan
; APPLICANT: LIAN, Ying
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE
; TITLE OF INVENTION: TYPE C POLYPEPTIDES, POLYPEPTIDES AND USE;
; FILE REFERENCE: 2302-18702 / 18702.002
; CURRENT APPLICATION NUMBER: US/10/190,305A
; CURRENT FILING DATE: 2002-07-05
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SEQ ID NO 15
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Matches 1477; Conservative
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Sequence 9, Application US/10190435
; Publication No. US20030143248A1
; GENERAL INFORMATION:
APPLICANT: ZUR MEGEDE, Jan
APPLICANT: LIAN, Ying
APPLICANT: ENGELBRECHT, Susan W.
APPLICANT: VAN RENSBURG, Estrelita J.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
TITLE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF
FILE REFERENCE: PP18133.003 / 2302-18133
CURRENT APPLICATION NUMBER: US/10/190,435
CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 319
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO
; SEQ ID NO
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
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                                  CTGGCCGAGGCGATGAGCCAGGCCAACACCAGCGTGATGATGCAGAAGAGCAACTTCAAG
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            CTGGCCGAGGCGATGAGCCAGGCCAACACCAGCGTGATGATGCAGAAGAGCAACTTCAAG
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1447 CTGAAGAGCCTGTTCGGCAACGACCCCCTGAGCCAAGAA 1485	1441 CTGAAGAGCCTGTTCGGCAACGACCCCCTGAGCCAGTAA 1479	1387 TTCGAGGAGACCACCCCGGCCAGAAGCAGGAGAGCAAGGACCGCGAGACCCTGACCAGC 1446	1381 TTCGAGGAGACCACCCCCGGCCAGAAGCAGGAGGAAGGACCGCGAGAGCCCTGACCAGC 1440	1327 CCCGGCAACTTCCTGCAGAGCCGCCCCGAGCCCACCGCCCCCCCGCGAGAGCTTCCGC 1386	1321 CCCGGCAACTTCCTGCAGAGCCGCCCCGAGCCCACCGCCCCCCCC	1267 GACTGCACCGAGCCCAGGCCAACTTCCTGGGCAAGATCTGGCCCAGCCACAAGGGCCGC 1326	1261 GACTGCACCGAGCGCCAGGCCAACTTCCTGGGCAAGATCTGGCCCAGGCCACAAAGGGCCGC 1320	1207 TGCCGCCCCCCCCCCCCAAGAAGGGCTGCTGGAAGTGCGGCAAGGAGGGCCACCAGATGAAG 1266	1201 TGCCGCGCCCCCCGCAAGAAGGGCTGCTGGAAGTGCGGCAAGGAGGGCCACCAGATGAAG 1260	1147 GGCCCCCGGCGATCGTCAAGTGCTTCAACTGCGGCAAGGAGGGCCACATCGCCCGCAAC 1206	1141 GGCCCCCGGCGCATCGTCAAGTGCTTCAACTGCGGCAAGGAGGGCCACATCGCCCGCAAC 1200

Search completed: March 13, 2005, 04:29:36 Job time: 901.894 secs

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